

Db 241 IASTKICNNKILWLCSEFMSLWAGSKNNQSRMDVYMSHAPTSSVHNLHIKQLYH 300
QY 301 SDEFRAYDGNADNKKHYNQSHPPYDITAMKVPYTAIWAGGHVLTGTPQDVARIILPQIK 360
Db 301 SDEFRAYDGNADNKKHYNQSHPPYDITAMKVPYTAIWAGGHVLTGTPQDVARIILPQIK 360
QY 361 SLVLVLSLPEWPTDFVWGLDAPQRMFSGNHL 395
Db 361 SLVLVLSLPEWPTDFVWGLDAPQRMFSGNHL 395

RESULT 2
US-10-056-744B-2
; Sequence 2, Application US/10056744B
; Publication No. US20020193303A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL ESTER
; FILE REFERENCE: HYDROLASE AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/10/056,744B
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-744B-2

Query Match 95.08; Score 2030; DB 9; Length 398;
Best Local Similarity 97.28; Pred. No. 7.1e-194;
Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

QY 1 MWLLLTTCICGTLNAGGFLDLENEVPEVMNTSEIIYNGYPSEYEVTTEDGYIL 60
Db 1 MWLLLTTCICGTLNAGGFLDLENEVPEVMNTSEIIYNGYPSEYEVTTEDGYIL 60
QY 61 LVNRIPIGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120
Db 61 LVNRIPIGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120
QY 121 GNTWSRRHKTLSSETDEKFWAFSFDMAKYDLPVGTDFVNTKGTQEKLYFIGHSLGTTIGF 180
Db 121 GNTWSRRHKTLSSETDEKFWAFSFDMAKYDLPVGTDFVNTKGTQEKLYFIGHSLGTTIGF 180
QY 181 VAFSTMPELAQRKKNFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240
Db 181 VAFSTMPELAQRKKNFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240
QY 241 IASTKICNNKILWLCSEFMSLWAGSKNNQSRMDVYMSHAPTSSVHNLHIKQLYH 300
Db 241 IASTKICNNKILWLCSEFMSLWAGSKNNQSRMDVYMSHAPTSSVHNLHIKQLYH 300
QY 301 SDEFRAYDGNADNKKHYNQSHPPYDITAMKVPYTAIWAGGHVLTGTPQDVARIILPQIK 360
Db 301 SDEFRAYDGNADNKKHYNQSHPPYDITAMKVPYTAIWAGGHVLTGTPQDVARIILPQIK 360
QY 361 SLVLVLSLPEWPTDFVWGLDAPQRMFSGNHL 395
Db 361 SLH-YFKLLPDNN-HDFVWGLDAPQRMYS 388

RESULT 3
US-10-003-302-4
; Sequence 4, Application US/10003302
; Patent No. US20020142435A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; FILE REFERENCE: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01186DIV
; CURRENT APPLICATION NUMBER: US/10/003,302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-302-4

Query Match 51.3%; Score 1097; DB 12; Length 392;
Best Local Similarity 53.6%; Pred. No. 5.5e-101;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;

QY 2 MWLLLTTCICGTLNAGGFLDLENEVPEVMNTSEIIYNGYPSEYEVTTEDGYIL 61
Db 1 MRFLGLVCLVLTLSHSGGKLTAVDPETNNMVSEIIISYMGFPSEYLVETEDGYIL 60
QY 62 VNRIPYGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 121
Db 61 LNRIPYGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120
QY 122 NTSWRRHKTLSSETDEKFWAFSFDMAKYDLPVGTDFVNTKGTQEKLYFIGHSLGTTIGF 181
Db 121 NTSWRRHKTLSSETDEKFWAFSFDMAKYDLPVGTDFVNTKGTQEKLYFIGHSLGTTIGF 180
QY 182 AFSTMPELAQRKKNFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 241
Db 181 AFSTMPELAQRKKNFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240
QY 242 ASTKICNNKILWLCSEFMSLWAGSKNNQSRMDVYMSHAPTSSVHNLHIKQLYH 301
Db 241 LGTHVCTHVLKELCGNLCLFCFNERNLNMSRVDVITTHSPAGTSVQNMHLWSQAVFK 300
QY 302 DEFRAYDGNADNKKHYNQSHPPYDITAMKVPYTAIWAGGHVLTGTPQDVARIILPQIK 361
Db 301 QKQFADWGSASAKYFYHNSYPTTYNVKMDLVPTAVWSGGHDLADYDYNILLTQITN 360
QY 362 LSLVLSLPEWPTDFVWGLDAPQRMFSGNHL 395
Db 361 LVFPHES-IPWE-HLDFWGLDAPWRLYNTIINL 392

RESULT 4
US-10-042-431-41
; Sequence 41, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; FILE REFERENCE: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-431-41

Query Match 51.1%; Score 1091; DB 9; Length 399;
Best Local Similarity 53.3%; Pred. No. 2.2e-100;

XX Claim 1: Fig 2; 68pp; English.
 XX
 CC The present invention provides the protein, coding and genomic sequences
 CC of a human lysosomal acid lipase. The sequences can be used in the
 CC identification of modulators of lipase activity in cells and tissues that
 CC express the lipase, particularly the severe infantile-onset Wolman
 CC disease and the milder late-onset cholesteryl ester storage disease
 CC (CESD), which are caused by mutations in different parts of the lysosomal
 CC acid lipase (LIPA) gene. The present sequence is the protein of the
 CC invention.
 XX
 SQ Sequence 395 AA;
 Query Match 100.0%; Score 2137; DB 23; Length 395;
 Best Local Similarity 100.0%; Pred. No. 3.4e-206;
 Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMWLLTTTCLICGTLNAGGFLDLENEVPVWMTSEIIYNGYPSSEVEVTEGYIL 60
 DB 1 MMWLLTTTCLICGTLNAGGFLDLENEVPVWMTSEIIYNGYPSSEVEVTEGYIL 60
 QY 61 LVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDWMGNSR 120
 DB 61 LVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDWMGNSR 120
 QY 121 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPGVDFIVNKTGOEKLIFGHSLGTTIGF 180
 DB 121 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPGVDFIVNKTGOEKLIFGHSLGTTIGF 180
 QY 181 VAFSTPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240
 DB 181 VAFSTPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240
 QY 241 IASTKICNNKILWILICSEFMSLWAGSNKNNQSRMDVYMSHAPTGSVHNILHIKOLYH 300
 DB 241 IASTKICNNKILWILICSEFMSLWAGSNKNNQSRMDVYMSHAPTGSVHNILHIKOLYH 300
 QY 301 SDEFRAYDNGNDADNMKHYNQSHPPYIDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 360
 DB 301 SDEFRAYDNGNDADNMKHYNQSHPPYIDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 360
 QY 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFSGNHNL 395
 DB 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFSGNHNL 395

RESULT 2
 AAU98539
 ID AAU98539 standard; Protein; 427 AA.
 XX
 AC AAU98539;
 XX
 XX 21-AUG-2002 (first entry)
 XX
 DE Human lysosomal acid lipase protein #2.
 XX
 KW Human; lysosomal acid lipase; cancer; CNS; obesity; chromosome 10;
 KW central nervous system disorder; chronic obstructive pulmonary disease;
 KW diabetes; cardiovascular disorder; Alzheimer's disease; dementia;
 KW Parkinson's disease; multiple sclerosis; Huntington's disease; pain;
 KW congestive heart failure; myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200236754-A2.
 XX
 PD 10-MAY-2002.
 XX
 XX 26-OCT-2001; 2001WO-EP12382.
 XX
 XX 31-OCT-2000; 2000US-244215P.
 XX
 XX 06-DEC-2000; 2000US-251401P.

XX (FARB) BAYER AG.
 XX
 PI Xiao Y;
 XX
 DR WPI: 2002-490007/52.
 DR N-PSDB; ABK85978.
 XX
 PT Novel human lysosomal acid lipase polypeptide, useful for treating
 PT cancer, central nervous system disorder, obesity, chronic obstructive
 PT pulmonary disease, diabetes or cardiovascular disorder
 XX
 PS Claim 1; Fig 5; 126pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of a purified
 CC human lysosomal acid lipase protein. The sequences of the invention are
 CC useful for screening for agents which modulate the activity of human
 CC lysosomal acid lipase polypeptide. A compound which increases human
 CC lysosomal acid lipase activity may be identified as a potential
 CC therapeutic agent for increasing the activity of the human lysosomal
 CC acid lipase, and a test compound which decreases the human lysosomal
 CC acid lipase activity is identified as a potential therapeutic agent for
 CC decreasing the activity of human lysosomal acid lipase. A pharmaceutical
 CC compound containing the lysosomal acid lipase sequences is useful for
 CC the preparation of a medicament for modulating the activity of human
 CC lysosomal acid lipase in a disease such as cancer, central nervous
 CC system (CNS) disorder, obesity, chronic obstructive pulmonary disease,
 CC diabetes or a cardiovascular disorder. A reagent that modifies the
 CC activity of the protein of the invention is useful for treating a human
 CC lysosomal acid lipase dysfunction related disease, preferably the above
 CC mentioned diseases. A DNA or protein sequence of the invention is
 CC useful for treating the above mentioned disorders, where the CNS
 CC disorders are selected from Alzheimer's and Parkinson's disease,
 CC dementia, multiple sclerosis, Huntington's disease, and pain, and the
 CC cardiovascular disorder is selected from congestive heart failure and
 CC myocardial infarction. The present sequence represents a human lysosomal
 CC acid lipase protein of the invention, the gene encoding this protein is
 CC located on human chromosome 10.
 XX
 SQ Sequence 427 AA;
 Query Match 95.0%; Score 2030; DB 23; Length 427;
 Best Local Similarity 97.2%; Pred. No. 2.2e-195;
 Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;
 QY 1 MMWLLTTTCLICGTLNAGGFLDLENEVPVWMTSEIIYNGYPSSEVEVTEGYIL 60
 DB 30 MMWLLTTTCLICGTLNAGGFLDLENEVPVWMTSEIIYNGYPSSEVEVTEGYIL 89
 QY 61 LVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDWMGNSR 120
 DB 90 LVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDWMGNSR 149
 QY 121 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPGVDFIVNKTGOEKLIFGHSLGTTIGF 180
 DB 150 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPGVDFIVNKTGOEKLIFGHSLGTTIGF 209
 QY 181 VAFSTPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240
 DB 210 VAFSTPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 269
 QY 241 IASTKICNNKILWILICSEFMSLWAGSNKNNQSRMDVYMSHAPTGSVHNILHIKOLYH 300
 DB 270 IASTKICNNKILWILICSEFMSLWAGSNKNNQSRMDVYMSHAPTGSVHNILHIKOLYH 329
 QY 301 SDEFRAYDNGNDADNMKHYNQSHPPYIDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 360
 DB 330 SDEFRAYDNGNDADNMKHYNQSHPPYIDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 389
 QY 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFS 390
 DB 390 SLH-YFKLLPDWN-HFDVWGLDAPQRMYS 417


```

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001186DIV
; CURRENT APPLICATION NUMBER: US/10/003,302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-003-302-4

Query Match      51.3%; Score 1097; DB 12; Length 392;
Best Local Similarity 53.6%; Pred. No. 5.5e-101;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;

QY 2 MWLLTTTCLICGTNLAGGFLDLENEVNPVMMNTSEIIYNGPSEYEVTTEDGYIL 61
Db 1 MRFLGLVCLVLTLSHSEGGKLTAVDPETNMVSEIIYWGPPSEYLVETEDGYIL 60
QY 62 VNRIPYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLLDAGYDVWNGSR 121
Db 61 LNRIPHGKRNHSDKPKPVVFLQHGILLADSSNWTNLANSLSGLFLLADAGFDVWNGSR 120
QY 122 NTWSRRHKTLSSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTTIGF 181
Db 121 NTWSRRHKTLSVSQDFWAFSDEMAYDLPASINFILNKTGQEQVYVGHSGTTIGFI 180
QY 182 AFSTMPELAQRKMNKFNALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 241
Db 181 AFSTMPELAQRKMNKFNALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
QY 242 ASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKOLYH 301
Db 241 LGTHVCHTHVILKCGNLCLFLLCGFNERNLNMSRDVYTHSPAGTSVQNNLHWSQAVKE 300
QY 302 DEFRAIDMGNDADNNKHYNQSHPPYDITAMKVPTAIWAGGHDLVLTQDVARILPQIK 361
Db 301 QKQAFDNGSSAKNYFHYNQSYPTYNVKMLVPTAVWNGHDLADYDVNILLTQITN 360
QY 362 LSLVLSLLPEWEPPTDFVWGLDAPQRMFSGNHL 395
Db 361 LVFHES-IPWE-HLDFIWGLDAPWRLYNKIINL 392

RESULT 4
US-10-042-431-41
; Sequence 41, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-6U2
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-042-431-41

Query Match      51.1%; Score 1091; DB 9; Length 399;
Best Local Similarity 53.3%; Pred. No. 2.2e-100;

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001186DIV
; CURRENT APPLICATION NUMBER: US/10/003,302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-003-302-4

Query Match      95.0%; Score 2030; DB 9; Length 398;
Best Local Similarity 97.2%; Pred. No. 7.1e-194;
Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

QY 1 MWLLTTTCLICGTNLAGGFLDLENEVNPVMMNTSEIIYNGPSEYEVTTEDGYIL 60
Db 1 MWLLTTTCLICGTNLAGGFLDLENEVNPVMMNTSEIIYNGPSEYEVTTEDGYIL 60
QY 61 LVNRIYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLLDAGYDVWNGSR 120
Db 61 LVNRIYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLLDAGYDVWNGSR 120
QY 121 GNTWSRRHKTLSSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTTIGF 180
Db 121 GNTWSRRHKTLSSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTTIGF 180
QY 181 VAFSTMPELAQRKMNKFNALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
Db 181 VAFSTMPELAQRKMNKFNALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
QY 241 IASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKOLYH 300
Db 241 IASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKOLYH 300
QY 301 SDEFRAIDMGNDADNNKHYNQSHPPYDITAMKVPTAIWAGGHDLVLTQDVARILPQIK 360
Db 301 SDEFRAIDMGNDADNNKHYNQSHPPYDITAMKVPTAIWAGGHDLVLTQDVARILPQIK 360
QY 361 LSLVLSLLPEWEPPTDFVWGLDAPQRMFS 390
Db 361 SLH-YFKLLPDWN-HDFVWGLDAPQRMYS 388

RESULT 3
US-10-003-302-4
; Sequence 4, Application US/10003302
; Patent No. US20020142435A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
```

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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001186DIV
; CURRENT APPLICATION NUMBER: US/10/003,302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-003-302-4

Query Match      51.3%; Score 1097; DB 12; Length 392;
Best Local Similarity 53.6%; Pred. No. 5.5e-101;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;

QY 2 MWLLTTTCLICGTNLAGGFLDLENEVNPVMMNTSEIIYNGPSEYEVTTEDGYIL 61
Db 1 MRFLGLVCLVLTLSHSEGGKLTAVDPETNMVSEIIYWGPPSEYLVETEDGYIL 60
QY 62 VNRIPYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLLDAGYDVWNGSR 121
Db 61 LNRIPHGKRNHSDKPKPVVFLQHGILLADSSNWTNLANSLSGLFLLADAGFDVWNGSR 120
QY 122 NTWSRRHKTLSSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTTIGF 181
Db 121 NTWSRRHKTLSVSQDFWAFSDEMAYDLPASINFILNKTGQEQVYVGHSGTTIGFI 180
QY 182 AFSTMPELAQRKMNKFNALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 241
Db 181 AFSTMPELAQRKMNKFNALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
QY 242 ASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKOLYH 301
Db 241 LGTHVCHTHVILKCGNLCLFLLCGFNERNLNMSRDVYTHSPAGTSVQNNLHWSQAVKE 300
QY 302 DEFRAIDMGNDADNNKHYNQSHPPYDITAMKVPTAIWAGGHDLVLTQDVARILPQIK 361
Db 301 QKQAFDNGSSAKNYFHYNQSYPTYNVKMLVPTAVWNGHDLADYDVNILLTQITN 360
QY 362 LSLVLSLLPEWEPPTDFVWGLDAPQRMFSGNHL 395
Db 361 LVFHES-IPWE-HLDFIWGLDAPWRLYNKIINL 392

RESULT 4
US-10-042-431-41
; Sequence 41, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-6U2
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-042-431-41

Query Match      51.1%; Score 1091; DB 9; Length 399;
Best Local Similarity 53.3%; Pred. No. 2.2e-100;

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001186DIV
; CURRENT APPLICATION NUMBER: US/10/003,302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-003-302-4
```


XX PS Claim 1; Fig 2; 68pp; English.

XX CC The present invention provides the protein, coding and genomic sequences

CC of a human lysosomal acid lipase. The sequences can be used in the

CC identification of modulators of lipase activity in cells and tissues that

CC express the lipase, particularly the severe infantile-onset Wolman

CC disease and the milder late-onset cholesteryl ester storage disease

CC (CESD), which are caused by mutations in different parts of the lysosomal

CC acid lipase (LIPA) gene. The present sequence is the protein of the

XX CC invention.

XX PS Sequence 395 AA;

XX CC Query Match 100.0%; Score 2137; DB 23; Length 395;

CC Best Local Similarity 100.0%; Pred. No. 3.4e-206;

XX CC Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWLLTTTCLICGTLNAGGFLDLENEVPEVNMNTSEIIYNGYSPSEEVETDGYIL 60

DB 1 MMWLLTTTCLICGTLNAGGFLDLENEVPEVNMNTSEIIYNGYSPSEEVETDGYIL 60

QY 61 LVNRIPIGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120

DB 61 LVNRIPIGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120

QY 121 GNTWSRRHKTSETDEKFWAFSEDEMAKYDLPGVDFIVNKTGQEKLYFTGHSLGTIGF 180

DB 121 GNTWSRRHKTSETDEKFWAFSEDEMAKYDLPGVDFIVNKTGQEKLYFTGHSLGTIGF 180

QY 181 VAFSTPELAQRKIMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFLEDKTK 240

DB 181 VAFSTPELAQRKIMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFLEDKTK 240

QY 241 IASTKICNNKILWILICSEFMSLWAGSNKKNQSRMDVYMSHAPTGSVHNILHIKOLYH 300

DB 241 IASTKICNNKILWILICSEFMSLWAGSNKKNQSRMDVYMSHAPTGSVHNILHIKOLYH 300

QY 301 SDEFRAYDNGNDADNMKHNQSHPIYDLTAMKVPTAIWAGGHVDVLTGPQDVARILPOIK 360

DB 301 SDEFRAYDNGNDADNMKHNQSHPIYDLTAMKVPTAIWAGGHVDVLTGPQDVARILPOIK 360

QY 361 SLSLVSLPPEWETFDVWGLDAPQRMFSGNHL 395

DB 361 SLSLVSLPPEWETFDVWGLDAPQRMFSGNHL 395

RESULT 2

AAU98539

ID AAU98539 standard; Protein; 427 AA.

XX AC AAU98539;

XX XX 21-AUG-2002 (first entry)

DT Human lysosomal acid lipase protein #2.

DE

XX Human; lysosomal acid lipase; cancer; CNS; obesity; chromosome 10;

XX central nervous system disorder; chronic obstructive pulmonary disease;

KW diabetes; cardiovascular disorder; Alzheimer's disease; dementia;

KW Parkinson's disease; multiple sclerosis; Huntington's disease; pain;

KW congestive heart failure; myocardial infarction.

XX OS Homo sapiens.

XX PN WO200236754-A2.

XX PN 10-MAY-2002.

XX PD 26-OCT-2001; 2001WO-EPI2382.

XX PF 31-OCT-2000; 2000US-244215P.

XX PR 06-DEC-2000; 2000US-251401P.

XX PA (FARB) BAYER AG.

XX PI xiao Y;

XX WPI: 2002-490007/52.

DR N-PSDB; ABK85978.

XX Novel human lysosomal acid lipase polypeptide, useful for treating

PT cancer, central nervous system disorder, obesity, chronic obstructive

PT pulmonary disease, diabetes or cardiovascular disorder

XX Claim 1; Fig 5; 126pp; English.

XX This invention relates to the DNA and protein sequences of a purified

CC human lysosomal acid lipase protein. The sequences of the invention are

CC useful for screening for agents which modulate the activity of human

CC lysosomal acid lipase polypeptide. A compound which increases human

CC lysosomal acid lipase activity may be identified as a potential

CC therapeutic agent for increasing the activity of the human lysosomal

CC acid lipase, and a test compound which decreases the human lysosomal

CC acid lipase activity is identified as a potential therapeutic agent for

CC decreasing the activity of human lysosomal acid lipase. A pharmaceutical

CC compound containing the lysosomal acid lipase sequences is useful for

CC the preparation of a medicament for modulating the activity of human

CC lysosomal acid lipase in a disease such as cancer, central nervous

CC system (CNS) disorder, obesity, chronic obstructive pulmonary disease,

CC diabetes or a cardiovascular disorder. A reagent that modifies the

CC activity of the protein of the invention is useful for treating a human

CC lysosomal acid lipase dysfunction related disease, preferably the above

CC mentioned diseases. A DNA or protein sequence of the invention is

CC useful for treating the above mentioned disorders, where the CNS

CC disorders are selected from Alzheimer's and Parkinson's disease,

CC dementia, multiple sclerosis, Huntington's disease, and pain, and the

CC cardiovascular disorder is selected from congestive heart failure and

CC myocardial infarction. The present sequence represents a human lysosomal

CC acid lipase protein of the invention, the gene encoding this protein is

CC located on human chromosome 10.

XX Sequence 427 AA;

XX Query Match 95.0%; Score 2030; DB 23; Length 427;

CC Best Local Similarity 97.2%; Pred. No. 2.2e-195;

XX CC Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

QY 1 MMWLLTTTCLICGTLNAGGFLDLENEVPEVNMNTSEIIYNGYSPSEEVETDGYIL 60

DB 30 MMWLLTTTCLICGTLNAGGFLDLENEVPEVNMNTSEIIYNGYSPSEEVETDGYIL 89

QY 61 LVNRIPIGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120

DB 90 LVNRIPIGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 149

QY 121 GNTWSRRHKTSETDEKFWAFSEDEMAKYDLPGVDFIVNKTGQEKLYFTGHSLGTIGF 180

DB 150 GNTWSRRHKTSETDEKFWAFSEDEMAKYDLPGVDFIVNKTGQEKLYFTGHSLGTIGF 209

QY 181 VAFSTPELAQRKIMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFLEDKTK 240

DB 210 VAFSTPELAQRKIMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFLEDKTK 269

QY 241 IASTKICNNKILWILICSEFMSLWAGSNKKNQSRMDVYMSHAPTGSVHNILHIKOLYH 300

DB 270 IASTKICNNKILWILICSEFMSLWAGSNKKNQSRMDVYMSHAPTGSVHNILHIKOLYH 329

QY 301 SDEFRAYDNGNDADNMKHNQSHPIYDLTAMKVPTAIWAGGHVDVLTGPQDVARILPOIK 360

DB 330 SDEFRAYDNGNDADNMKHNQSHPIYDLTAMKVPTAIWAGGHVDVLTGPQDVARILPOIK 389

QY 361 SLSLVSLPPEWETFDVWGLDAPQRMFS 390

DB 390 SLH-YFKLLPDWN-HFEVWGLDAPQRMYS 417

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:35:22 ; Search time 77 seconds
(without alignments)
683.558 Million cell updates/sec

Title: US-10-003-302-2

Perfect score: 2137

Sequence: 1 MMWLLFTTCLICGTNAGG.....FDFWGLDAPQRMFSGNHL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2137	100.0	395	AAO18226	Human lysosomal ac
2	2030	95.0	427	AAU98539	Human lysosomal ac
3	2009	94.0	403	AAU77493	Human lipid metabo
4	1823	85.3	365	AAE17307	Human lysosomal ac
5	1242	58.1	397	AAE17308	Human lysosomal ac
6	1108	51.8	311	AAU98540	Human lysosomal ac
7	1097	51.3	392	AAO18227	Human lysosomal ac
8	1091	51.1	399	AAU90783	Human shear stress
9	1091	51.1	399	AAU90783	Human lysosomal ac
10	1052	49.2	398	7 AAP60724	Sequence of pregas

11	1052	49.2	398	7 AAP60658	Sequence of human
12	1052	49.2	398	17 AAU09383	Human gastric lipa
13	1052	49.2	398	22 AAB66086	Human lipase prote
14	1031	48.2	409	22 AAE11931	Human CGI62 (or C5
15	1031	48.2	423	22 AAB66065	Human TANGO 294.
16	1030	48.2	395	23 AAE14744	Human triacylglyce
17	1030	48.2	399	23 AAU77496	Human lipid metabo
18	1027	48.1	398	14 AAU37302	RGL precursor. Or
19	1026	48.0	399	22 AAG67513	Amino acid sequenc
20	1023	47.9	390	22 AAB66067	Human TANGO 294 ma
21	1014.5	47.5	395	6 AAP50322	Rat lingual lipase
22	1004	47.0	379	15 AAR56870	Canine gastric lip
23	1004	47.0	379	17 AAU09382	Dog gastric lipase
24	1004	47.0	380	15 AAR56871	Canine gastric lip
25	995	46.6	398	23 AAU99164	Human lysosomal ac
26	989.5	46.3	449	22 AAU30498	Novel human secret
27	972	45.5	378	23 ABB76189	Kid goat pregastr
28	913.5	42.7	371	23 AAU99165	Human lysosomal ac
29	798	37.3	731	23 AAE14746	Human triacylglyce
30	723	33.8	276	23 AAE14745	Human triacylglyce
31	723	33.8	289	23 AAU77494	Human lipid metabo
32	700	32.8	221	22 AAB66068	Human TANGO 294 ex
33	672.5	31.5	280	23 AAE14743	Human triacylglyce
34	661.5	31.0	656	22 ABB66839	Novel human diagno
35	643	30.1	233	22 AAB61608	Human protein HP03
36	561.5	26.3	399	22 ABB71442	Drosophila melanog
37	548.5	25.7	434	22 ABB62081	Drosophila melanog
38	546	25.5	456	22 ABB68957	Drosophila melanog
39	542.5	25.4	398	22 ABB63011	Drosophila melanog
40	533	24.9	394	22 ABB71702	Drosophila melanog
41	511.5	23.9	416	22 ABB59328	Drosophila melanog
42	508	23.8	457	22 ABB63187	Drosophila melanog
43	496.5	23.2	410	21 AAY32309	Soybean acid triac
44	495	23.2	435	22 ABB71506	Drosophila melanog
45	492.5	23.0	410	21 AAY32307	Rice acid triacylg

ALIGNMENTS

RESULT 1
AAO18226
ID AAO18226 standard; Protein; 395 AA.

XX AC AAO18226;
XX DT 18-SEP-2002 (first entry)

XX DE Human lysosomal acid lipase.

XX KW Human; lysosomal acid lipase; chromosome 10; lipemic; Wolman disease; cholesteryl ester storage disease.

XX OS Homo sapiens.

XX PN USG387680-B1.

XX PD 14-MAY-2002.

XX PF 29-MAR-2001; 2001US-0820001.

XX PR 29-MAR-2001; 2001US-0820001.

XX PA (PEKE) PE CORP NY.

XX PI Merkulo GV, Ketchum KA, Di Francesco V, Beasley EM;

XX DR WPI; 2002-478445/51.

XX DR N-PSDB; AAL47480, AAL47481.

XX PT Isolated nucleic acids encoding a lysosomal acid lipase protein useful for the prevention, diagnosis and treatment of severe infantile-onset Wolman disease and late-onset cholesteryl ester storage disease

```
XX Claim 1; Fig 2; 68pp; English.
XX
CC The present invention provides the protein, coding and genomic sequences
CC of a human lysosomal acid lipase. The sequences can be used in the
CC identification of modulators of lipase activity in cells and tissues that
CC express the lipase, particularly the severe infantile-onset Wolman
CC disease and the milder late-onset cholesteryl ester storage disease
CC (CESD), which are caused by mutations in different parts of the lysosomal
CC acid lipase (LIPA) gene. The present sequence is the protein of the
CC invention.
XX
XX Sequence 395 AA;
XX
XX Query Match 100.0%; Score 2137; DB 23; Length 395;
XX Best Local Similarity 100.0%; Pred. No. 3.4e-206;
XX Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MMWLLTTTCLICGTNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTTEDGYIL 60
DB 1 MMWLLTTTCLICGTNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTTEDGYIL 60
QY 61 LVNRIPIYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120
DB 61 LVNRIPIYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120
QY 121 GNTWSRRHKTSETDEKFWAFSDEMAYDLPVDFIVNKTGOEKLFIHSLGTTIGF 180
DB 121 GNTWSRRHKTSETDEKFWAFSDEMAYDLPVDFIVNKTGOEKLFIHSLGTTIGF 180
QY 181 VAFSTMPPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
DB 181 VAFSTMPPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
QY 241 IASTKICNNKILWLICSEFMSLWAGSNKKNMQSRMDVYMSHAPTGSVHNHLIKQLYH 300
DB 241 IASTKICNNKILWLICSEFMSLWAGSNKKNMQSRMDVYMSHAPTGSVHNHLIKQLYH 300
QY 301 SDEFRAYDNGNDADNKKHYNQSHPPIDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 360
DB 301 SDEFRAYDNGNDADNKKHYNQSHPPIDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 360
QY 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFSGNHNL 395
DB 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFSGNHNL 395
XX
RESULT 2
AAU98539
ID AAU98539 standard; Protein; 427 AA.
XX
AC AAU98539;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human lysosomal acid lipase protein #2.
XX
KW Human; lysosomal acid lipase; cancer; CNS; obesity; chromosome 10;
KW central nervous system disorder; chronic obstructive pulmonary disease;
KW diabetes; cardiovascular disorder; Alzheimer's disease; dementia;
KW Parkinson's disease; multiple sclerosis; Huntington's disease; pain;
KW congestive heart failure; myocardial infarction.
XX
OS Homo sapiens.
XX
XX WO200236754-A2.
XX
PN 10-MAY-2002.
XX
PD 26-OCT-2001; 2001WO-EP12382.
XX
PF 31-OCT-2000; 2000US-244215P.
XX
PR 06-DEC-2000; 2000US-251401P.
```

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XX (FARB ) BAYER AG.
XX
XX Xiao Y;
XX
XX WPI: 2002-490007/52.
XX N-PSDB; ABK85978.
XX
XX Novel human lysosomal acid lipase polypeptide, useful for treating
XX cancer, central nervous system disorder, obesity, chronic obstructive
XX pulmonary disease, diabetes or cardiovascular disorder
XX
XX Claim 1; Fig 5; 126pp; English.
XX
XX This invention relates to the DNA and protein sequences of a purified
XX human lysosomal acid lipase protein. The sequences of the invention are
XX useful for screening for agents which modulate the activity of human
XX lysosomal acid lipase polypeptide. A compound which increases human
XX lysosomal acid lipase activity may be identified as a potential
XX therapeutic agent for increasing the activity of the human lysosomal
XX acid lipase, and a test compound which decreases the human lysosomal
XX acid lipase activity is identified as a potential therapeutic agent for
XX decreasing the activity of human lysosomal acid lipase. A pharmaceutical
XX compound containing the lysosomal acid lipase sequences is useful for
XX the preparation of a medicament for modulating the activity of human
XX lysosomal acid lipase in a disease such as cancer, central nervous
XX system (CNS) disorder, obesity, chronic obstructive pulmonary disease,
XX diabetes or a cardiovascular disorder. A reagent that modifies the
XX activity of the protein of the invention is useful for treating a human
XX lysosomal acid lipase dysfunction related disease, preferably the above
XX mentioned diseases. A DNA or protein sequence of the invention is
XX useful for treating the above mentioned disorders, where the CNS
XX disorders are selected from Alzheimer's and Parkinson's disease,
XX dementia, multiple sclerosis, Huntington's disease, and pain, and the
XX cardiovascular disorder is selected from congestive heart failure and
XX myocardial infarction. The present sequence represents a human lysosomal
XX acid lipase protein of the invention, the gene encoding this protein is
XX located on human chromosome 10.
XX
XX Sequence 427 AA;
XX
XX Query Match 95.0%; Score 2030; DB 23; Length 427;
XX Best Local Similarity 97.2%; Pred. No. 2.2e-195;
XX Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;
XX
QY 1 MMWLLTTTCLICGTNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTTEDGYIL 60
DB 30 MMWLLTTTCLICGTNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTTEDGYIL 89
QY 61 LVNRIPIYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120
DB 90 LVNRIPIYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 149
QY 121 GNTWSRRHKTSETDEKFWAFSDEMAYDLPVDFIVNKTGOEKLFIHSLGTTIGF 180
DB 150 GNTWSRRHKTSETDEKFWAFSDEMAYDLPVDFIVNKTGOEKLFIHSLGTTIGF 209
QY 181 VAFSTMPPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
DB 210 VAFSTMPPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 269
QY 241 IASTKICNNKILWLICSEFMSLWAGSNKKNMQSRMDVYMSHAPTGSVHNHLIKQLYH 300
DB 270 IASTKICNNKILWLICSEFMSLWAGSNKKNMQSRMDVYMSHAPTGSVHNHLIKQLYH 329
QY 301 SDEFRAYDNGNDADNKKHYNQSHPPIDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 360
DB 330 SDEFRAYDNGNDADNKKHYNQSHPPIDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 389
QY 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFS 390
DB 390 SLH-YFKLLLPDWN-HFDVWGLDAPQRMYS 417
```

RESULT 3

AAU77493
 ID AAU77493 standard; Protein; 403 AA.
 AC AAU77493;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human lipid metabolism enzyme, LMM-1.
 XX
 KW Human; lipid metabolism enzyme; LMM-1; immune system disorder;
 KW neurological disorder; developmental disorder; cancer; nootropic;
 KW cell proliferative disorder; immunomodulator; neuroprotective;
 KW cytosolic; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO200216597-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-AUG-2001; 2001WO-US26365.
 XX
 PR 23-AUG-2000; 2000US-227429P.
 PR 08-SEP-2000; 2000US-231370P.
 PR 15-SEP-2000; 2000US-233212P.
 PR 29-SEP-2000; 2000US-236885P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Griffin JA, Patterson C, Gandhi AR, Lu Y, Yao MG, Baughn MR;
 PI Walia NK, Hafalia AJA, Ding L, Tribouley CM, Das D, Thornton M;
 PI Lal P;
 XX
 DR WPI: 2002-280936/32.
 DR N-PSDB; ABK12385.
 XX
 PT New lipid metabolism enzymes, useful for diagnosing, treating or
 PT preventing immune system disorders (e.g. Crohn's disease), neurological
 PT disorders (e.g. Parkinson's disease), or cell proliferative disorders
 PT (e.g. cancers) -
 XX
 PS Claim 45; Page 108-109; 122pp; English.
 XX
 CC The present invention relates to the isolation of human lipid
 CC metabolism enzymes (LMM) designated LMM-1 to LMM-6, and the
 CC polynucleotide sequences encoding them. The LMM polypeptides,
 CC polynucleotides, agonists and antagonists are useful for diagnosing,
 CC treating or preventing disorders associated with aberrant expression
 CC of LMM, particularly immune system disorders (e.g. acquired
 CC immunodeficiency syndrome (AIDS), thymic hypoplasia, anaemia,
 CC asthma or Crohn's disease), neurological disorders (e.g. epilepsy,
 CC Huntington's disease, dementia or Parkinson's disease), developmental
 CC disorders (e.g. Down's syndrome) or cell proliferative disorders
 CC (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC myeloma or sarcoma). The present sequence represents human LMM-1.
 XX
 SQ Sequence 403 AA;
 Query Match 94.08; Score 2009; DB 23; Length 403;
 Best Local Similarity 96.24; Pred. No. 2.6e-193;
 Matches 375; Conservative 3; Mismatches 10; Indels 2; Gaps 2;
 1 MWLLLTTCICGTLAGGFLDLENEVNPVWMTSEIIYNGVPSSEYEVTTEDGVIL 60
 6 MWLLLTTCICGTLAGGFLDLENEVNPVWMTSEIIYNGVPSSEYEVTTEDGVIL 65
 61 LVNRIPIYGRTHARSTGRPPVVMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120
 66 LVNRIPIYGRTHARSTGRPPVVMQHALFAGQAYWLENYANGSLGFLADAGYDVMGNSR 125
 121 GNTWSRRHKLSETDEKFWAFSDEMAYDLPVGVDFIVNKTGQEKLYFIGHSLGTTIGF 180

Db 126 GNTWSRRHKLSETDEKFWAFSDEMAYDLPVGVDFIVNKTGQEKLYFIGHSLGTTIGF 185
 Qy 181 VAFSTMPPELAQRIKMNKMFALGPTISFKYPTGTFTRFELLPNLSLKAVFGTKGFLEDDKTK 240
 Db 186 VAFSTMPPELAQRIKMNKMFALGPTISFKYPTGTFTRFELLPNLSLKAVFGTKGFLEDDKTK 245
 Qy 241 IASTKICNNKIILWLCISFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKQLYH 300
 Db 246 IASTKICNNKIILWLCISFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKQLYH 305
 Qy 301 SDEFRAYDNGNDADNMKHYNQSHPPYDILTAMKVPTAIWAGHDVLGTPQDVARILPQIK 360
 Db 306 SDEFRAYDNGNDADNMKHYNQSHPPYDILTAMKVPTAIWAGHDVLGTPQDVARILPQIK 365
 Qy 361 SLSLVLSTLPEWETFEVWGLDAPQRMFS 390
 Db 366 SLH-YFKLLPDWN-HFDFVWGLDAPQRMYS 393
 RESULT 4
 AAEL17307
 ID AAEL17307 standard; Protein; 365 AA.
 AC AAEL17307;
 XX
 DT 18-APR-2002 (first entry)
 XX
 DE Human lysosomal acid lipase protein, sbg236015LIPASE #1.
 XX
 KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
 KW depression; cardiovascular disease; myocardial infarction; renal failure;
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
 KW hyperplenism; renal disease; hypoglycaemia; gastrointestinal disease;
 KW noctropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
 KW haemostatic; vulnery; anticonvulsant; antirheumatic; neuroprotective;
 KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
 KW allergy; lysosomal acid lipase.
 XX
 OS Homo sapiens.
 XX
 PN WO200198342-A1.
 XX
 PD 27-DEC-2001.
 XX
 PF 22-JUN-2001; 2001WO-US19929.
 XX
 PR 22-JUN-2000; 2000US-213156P.
 PR 22-JUN-2000; 2000US-213161P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
 PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
 XX
 DR WPI: 2002-139783/18.
 DR N-PSDB; AAD27802.
 XX
 PT Novel secreted and membrane-associated polypeptides and polynucleotides
 PT useful for preventing, ameliorating or correcting dysfunction or
 PT disease including diabetes, cancer, hypertension and growth
 PT abnormalities -
 XX
 PS Claim 1; Page 105; 138pp; English.
 XX
 CC The invention relates to secreted and membrane-associated polypeptides

CC and polynucleotides. The sequences of the invention are useful in
 CC diagnostic assays for detecting diseases associated with inappropriate
 CC activity or levels of these polynucleotides, and in identifying their
 CC agonists and antagonists that are potentially useful in therapy. The
 CC sequences of the invention are useful as vaccines for inducing
 CC immunological response. The sequences of the invention are useful for
 CC treating cancers, infections, autoimmune disorders, haematopoietic
 CC disorders, wound healing disorders, cholesteryl ester storage disease,
 CC inflammation, congenital muscular dystrophy, junctional epidermolysis
 CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
 CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
 CC allergies, schizophrenia, sbg42445PROA-associated disorders,
 CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
 CC graft versus host disease, ischaemia, stroke, acute respiratory disease
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
 CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
 CC depression, anxiety disorders and sleep disorders, cardiovascular
 CC diseases including congestive heart failure and myocardial infarction,
 CC respiratory diseases including chronic obstructive pulmonary disease,
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders
 CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
 CC and tendinitis, gastrointestinal diseases including intestinal
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
 CC reproductive diseases including low testosterone and male infertility.
 CC The present sequence is human lysosomal acid lipase.

XX Sequence 365 AA;

Query Match 85.3%; Score 1823; DB 23; Length 365;
 Best Local Similarity 88.9%; Pred No. 1, 2e-174;
 Matches 346; Conservative 2; Mismatches 7; Indels 34; Gaps 3;

QY 2 MWLLTTTCLICGTLNAGFLDLENEVPVNMNTSEIIYNGYPSEEVTTEDGYILL 61
 Db 1 MWLLTTTCLICGTLNAGFLDLENEVPVNMNTSEIIYNGYPSEEVTTEDGYILL 60
 QY 62 VNRIPYGRTHARSTGPRPVVWQHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
 Db 61 VNRIPYGRTHARST-----ADAGYDVMGNSRG 88
 QY 122 NTWSRRHKLSTDEKFWAFSEDEMAKYDLPGVDFIVNKTQGEKLYFGHSLGTTIGFV 181
 Db 89 NTWSRRHKLSTDEKFWAFSEDEMAKYDLPGVDFIVNKTQGEKLYFGHSLGTTIGFV 148
 QY 182 AFSTWPELAQRKMFALGPTISFYKPTGIFTRFELLPSIITKAVFGTKGFLEDKTKI 241
 Db 149 AFSTWPELAQRKMFALGPTISFYKPTGIFTRFELLPSIITKAVFGTKGFLEDKTKI 208
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 Db 209 ASTKICNNKILICSEFMSLWAGSNKKNMOSRMDVYMSHAPTSSVHNILHIKOLYHS 268
 QY 302 DEFRAYDNGNDADNNKHYNQSHPPYIDLTAMKVPTAINAGGHVDVLGTPODVARILPQIKS 361
 Db 269 DEFRAYDNGNDADNNKHYNQSHPPYIDLTAMKVPTAINAGGHVDVLGTPODVARILPQIKS 328
 QY 362 LSLVLSLLEPEWETTFDFVWGLDAPQRMFS 390
 Db 329 LH-YFKLLPDWN-HFDVWGLDAPQRMYS 355

RESULT 5
 ID AAEL17308 standard; Protein: 397 AA.
 XX AAEL17308;
 AC AAEL17308;

DT 18-APR-2002 (first entry)

XX

DE Human lysosomal acid lipase protein, sbg236015LIPASE #2.
 KW Human; therapy: wound healing disorder; vaccine; cancer; infection;
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
 KW depression; cardiovascular disease; myocardial infarction; renal failure;
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
 KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
 KW neutrotropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
 KW haemostatic; vulnerable; anticonvulsant; antirheumatic; neuroprotective;
 KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
 KW allergy; lysosomal acid lipase.
 XX Homo sapiens.
 XX WO200198342-A1.
 XX 27-DEC-2001.
 XX 22-JUN-2001; 2001WO-US19929.
 XX 22-JUN-2000; 2000US-213156P.
 XX 22-JUN-2000; 2000US-213161P.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
 PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
 DR WPI; 2002-139783/18.
 DR N-P5DB; AAD27803.
 PT Novel secreted and membrane-associated polypeptides and polynucleotides
 PT useful for preventing, ameliorating or correcting dysfunction or
 PT disease including diabetes, cancer, hypertension and growth
 PT abnormalities
 XX Claim 1; Page 106; 138pp; English.

The invention relates to secreted and membrane-associated polypeptides
 and polynucleotides. The sequences of the invention are useful in
 CC diagnostic assays for detecting diseases associated with inappropriate
 CC activity or levels of these polynucleotides, and in identifying their
 CC agonists and antagonists that are potentially useful in therapy. The
 CC sequences of the invention are useful as vaccines for inducing
 CC immunological response. The sequences of the invention are useful for
 CC treating cancers, infections, autoimmune disorders, haematopoietic
 CC disorders, wound healing disorders, cholesteryl ester storage disease,
 CC inflammation, congenital muscular dystrophy, junctional epidermolysis
 CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
 CC allergies, schizophrenia, sbg42445PROA-associated disorders,
 CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
 CC graft versus host disease, ischaemia, stroke, acute respiratory disease
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
 CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
 CC depression, anxiety disorders and sleep disorders, cardiovascular
 CC diseases including congestive heart failure and myocardial infarction,
 CC respiratory diseases including chronic obstructive pulmonary disease,
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders
 CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
 CC and tendinitis, gastrointestinal diseases including intestinal
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
 CC reproductive diseases including low testosterone and male infertility.

CC The present sequence is human lysosomal acid lipase protein.

XX Sequence 397 AA;

Query Match 58.1%; Score 1242; DB 23; Length 397;

Best Local Similarity 60.1%; Pred. No. 3.7e-116;

Matches 235; Conservative 49; Mismatches 101; Indels 6; Gaps 4;

Qy 2 MWLLITTC--LICGLNAGGFLDLENEVNPVWMTSEIIYNGYPSSEYEVTEDGYI 59

Db 1 MWQLLAACWMLLGSMY--GYDKGNANPEANNISQIISYWGYPSEYEDVTTKDGYI 58

Qy 60 LLVNRIPYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGLFLADAGYVWNGNS 119

Db 59 LGIYRIPHGRCPCGRTAPKPAVYLQHGGLIASASNNICLPNNSLAFLADSGYDVLGNS 118

Qy 120 RGNWRSRRHKTSETDEKFWAFSDEMAKYDLPGVDFIVNKTGOEKLYFIGHSLGTTIG 179

Db 119 RGNWRSRRHKTSETDEKFWAFSDEMAKYDLPATINFIIEKTKGRLYYVGHSGQTTIA 178

Qy 180 FVAFSTMPPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFLEDKKT 239

Db 179 FIAFSTNPELAKKIKIFALAPVTVKYTSQPMKLTLSRRVVKVLGDKMFPHTLFD 238

Qy 240 KIASTKICNNKILWICSEFSLWAGSNKKNMNSRMDVYMSHAPTGSSVHNILHIKOLY 299

Db 239 QFIATKVCNRKLFRRICSNFLTSLSGFDPQNLNMSRLDVYLSHNPAGTSVQNMLHWAQLY 298

Qy 300 HSDEFRAVDGNDADNMKHYNOSHPPYIDLTAMKVPTAIWAGGHVLTGTPQDVARILPQI 359

Db 299 HSDEFRAVDGNDADNMKHYNOSHPPYIDLTAMKVPTAIWAGGHVLTGTPQDVARILPQI 358

Qy 360 KSLSLVLSLLPEWEPTFDVFWGLDAPQRMFS 390

Db 359 KSLH-YFKLLPDWN-HFDVFWGLDAPQRMYS 387

RESULT 6

AAU98540

ID AAU98540 standard; Protein; 311 AA.

XX AAU98540;

AC AAU98540;

XX 21-AUG-2002 (first entry)

DE Human lysosomal acid lipase protein #3.

XX Human; lysosomal acid lipase; cancer; CNS; obesity; chromosome 10;

KW central nervous system disorder; chronic obstructive pulmonary disease;

KW diabetes; cardiovascular disorder; Alzheimer's disease; dementia;

KW Parkinson's disease; multiple sclerosis; Huntington's disease; pain;

KW congestive heart failure; myocardial infarction.

XX Homo sapiens.

OS WO200236754-A2.

XX 10-MAY-2002.

XX 26-OCT-2001; 2001WO-EPI2382.

XX 31-OCT-2000; 2000US-244215P.

PR 06-DEC-2000; 2000US-251401P.

XX (FARB) BAYER AG.

XX Xiao Y;

XX WPI; 2002-490007/52.

DR N-PSDB; ABK85969.

XX Novel human lysosomal acid lipase polypeptide, useful for treating

PT cancer, central nervous system disorder, obesity, chronic obstructive

PT pulmonary disease, diabetes or cardiovascular disorder

XX Claim 1; Fig 6; 126pp; English.

XX This invention relates to the DNA and protein sequences of a purified

CC human lysosomal acid lipase protein. The sequences of the invention are

CC useful for screening for agents which modulate the activity of human

CC lysosomal acid lipase polypeptide. A compound which increases human

CC lysosomal acid lipase activity may be identified as a potential

CC therapeutic agent for increasing the activity of the human lysosomal

CC acid lipase, and a test compound which decreases the human lysosomal

CC acid lipase activity is identified as a potential therapeutic agent for

CC decreasing the activity of human lysosomal acid lipase. A pharmaceutical

CC compound containing the lysosomal acid lipase sequences is useful for

CC the preparation of a medicament for modulating the activity of human

CC lysosomal acid lipase in a disease such as cancer, central nervous

CC system (CNS) disorder, obesity, chronic obstructive pulmonary disease,

CC diabetes or a cardiovascular disorder. A reagent that modifies the

CC activity of the protein of the invention is useful for treating a human

CC lysosomal acid lipase dysfunction related disease, preferably the above

CC mentioned diseases. A DNA or protein sequence of the invention is

CC useful for treating the above mentioned disorders, where the CNS

CC disorders are selected from Alzheimer's and Parkinson's disease,

CC dementia, multiple sclerosis, Huntington's disease, and pain, and the

CC cardiovascular disorder is selected from congestive heart failure and

CC myocardial infarction. The present sequence represents a human lysosomal

CC acid lipase protein of the invention, the gene encoding this protein is

CC located on human chromosome 10.

XX Query Match 51.8%; Score 1108; DB 23; Length 311;

Best Local Similarity 58.7%; Pred. No. 7.9e-103;

Matches 229; Conservative 11; Mismatches 32; Indels 118; Gaps 8;

Qy 1 MWLLITTCICGLNAGGFLDLENEVNPVWMTSEIIYNGYPSSEYEVTEDGYIL 60

Db 30 MWLLITTCICGLNAGGFLDLENEVNPVWMTSEIIYNGYPSSEYEVTEDGYIL 89

Qy 61 LVNRIPYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGLFLADAGYVWNGNSR 120

Db 90 LVNRIPYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGLFLADAGYVWNGNSR 149

Qy 121 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPGVDFIVNKTGOEKLYFIGHSLGTTIGF 180

Db 150 GNTWSRRHKTSETDEKFWAFRYTKG-----NAT----- 179

Qy 181 VAFSTMPPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFLEDKKTK 240

Db 180 -----AERAKOMEPGP----- 191

Qy 241 IASTKICNNKILWICSEFSLWAGSNKKNMNSRMDVYMSHAPTGSSVHNILHIKOLYH 300

Db 192 -----YWAIVDARESPFLFGNRE-----ESR-----GLKNT----- 217

Qy 301 SDEFRAVDGNDADNMKHYNOSHPPYIDLTAMKVPTAIWAGGHVLTGTPQDVARILPQIK 360

Db 218 ---QAYDWGNDADNMKHYNOSHPPYIDLTAMKVPTAIWAGGHVLTGTPQDVARILPQIK 273

Qy 361 SLSLVLSLLPEWEPTFDVFWGLDAPQRMFS 390

Db 274 SLH-YFKLLPDWN-HFDVFWGLDAPQRMYS 301

RESULT 7

AAO18227

ID AAO18227 standard; Protein; 392 AA.

XX AAO18227;

AC AAO18227;

XX 18-SEP-2002 (first entry)

XX Human lysosomal acid lipase related protein.

XX Human; lysosomal acid lipase; chromosome 10; lipemic; Wolman disease;
KW cholesteryl ester storage disease.
XX Homo sapiens.
XX US6387680-B1.
XX 14-MAY-2002.
XX 29-MAR-2001; 2001US-0820001.
XX 29-MAR-2001; 2001US-0820001.
XX (PEKE) PE CORP NY.
XX Merkulov GV, Ketchum KA, Di Francesco V, Beasley EM;
XX WPI; 2002-478445/51.
XX Isolated nucleic acids encoding a lysosomal acid lipase protein useful
PT for the prevention, diagnosis and treatment of severe infantile-onset
PT Wolman disease and late-onset cholesteryl ester storage disease -
XX Disclosure; Column 57-60; 68pp; English.
XX The present invention provides the protein, coding and genomic sequences
CC of a human lysosomal acid lipase. The sequences can be used in the
CC identification of modulators of lipase activity in cells and tissues that
CC express the lipase, particularly the severe infantile-onset Wolman
CC disease and the milder late-onset cholesteryl ester storage disease
CC (CESD), which are caused by mutations in different parts of the lysosomal
CC acid lipase (LIPA) gene. The present sequence is a protein shown in the
CC exemplification of the invention.
XX Sequence 392 AA;

Query Match 51.3%; Score 1097; DB 23; Length 392;
Best Local Similarity 53.6%; Pred. No. 1.4e-101;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;
QY 2 MWLLTTTCLICGTNAGGFLDENEVPEVMWNTSEIIYNGYPSEEVETEDGYILL 61
DB 1 MRFLGLVCLVWLTHSEGGGKLTAVDPETNMNVEIISYWGFFSEELVETEDGYILL 60
QY 62 VNRIPIYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
DB 61 LNRIPGRKNHSDKGPVFLQHLGLADSSNWVTNLANSSLGFLADAGYDVWNGNSRG 120
QY 122 NTSRRKHTLSTDEKFWAFSDENAKYDLPQVIDFIVNKTQOEKLYFTGHSLGTTIGFV 181
DB 121 NTSRRKHTLSVQDEFWAFSDENAKYDLPASINFILNKTQOEQVYVYGHSGQTTIGFI 180
QY 182 AFSTWPELAQRKMNPFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKKI 241
DB 181 AFSQIPELAKRIKMFALGPVAVAFCTSPMAKLGRLPDHLIKDLFGDKEFLPQSAFLKW 240
QY 242 ASTKICNNKILWLCIEFMSLWAGSNKKNMNQRMDVYMSHAPTSSSVHNILHIKQLYHS 301
DB 241 LGTHVCTHVILKELCNLCFLCGFNERNLNMRDVTYTHSPAGTSVQNMLHWSQAVKF 300
QY 302 DEFRAVDGNDADNMKHYNQSHPPYIDLTAMKVPTAIWAGGHDVLTGTPDVARILPQIKS 361
DB 301 QKFOAFDWGSSAKNFHYNQSPPTYNVKDMLVPTAVWSGGHDWLDVYDVNILLTQITN 360
QY 362 LSLVLSLLPEWPTDFVWGLDAPQRMFSGNHL 395
DB 361 LVFHES-IPWEH-HLDFIWGLDAPRWLNKIINL 392

RESULT 8
AAB90783
ID AAB90783 standard; Protein; 399 AA.

XX AAB90783;
XX 15-JUN-2001 (first entry)
XX Human shear stress-response protein SEQ ID NO: 66.
XX Human; shear stress-response protein; vascular disease;
XX arteriosclerosis.
XX Homo sapiens.
XX WO200125427-A1.
XX 12-APR-2001.
XX 02-OCT-2000; 2000WO-JP06840.
XX 01-OCT-1999; 99JP-0280976.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX (NOJI/) NOJIMA H.
XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX WPI; 2001-266308/27.
XX N-PSDB; AAH02906.
XX DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis -
XX Claim 60; Page 402-404; 678pp; Japanese.
XX The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension.
XX Sequence 399 AA;

Query Match 51.1%; Score 1091; DB 22; Length 399;
Best Local Similarity 53.3%; Pred. No. 5.7e-101;
Matches 210; Conservative 63; Mismatches 119; Indels 2; Gaps 2;
QY 2 MWLLTTTCLICGTNAGGFLDENEVPEVMWNTSEIIYNGYPSEEVETEDGYILL 61
DB 3 MRFLGLVCLVWLPHSEGGGKLTAVDPETNMNVEIISYWGFFSEELVETEDGYILL 62
QY 62 VNRIPIYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
DB 63 LNRIPGRKNHSDKGPVFLQHLGLADSSNWVTNLANSSLGFLADAGYDVWNGNSRG 122
QY 122 NTSRRKHTLSTDEKFWAFSDENAKYDLPQVIDFIVNKTQOEKLYFTGHSLGTTIGFV 181
DB 123 NTSRRKHTLSVQDEFWAFSDENAKYDLPASINFILNKTQOEQVYVYGHSGQTTIGFI 182
QY 182 AFSTWPELAQRKMNPFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKKI 241
DB 183 AFSQIPELAKRIKMFALGPVAVAFCTSPMAKLGRLPDHLIKDLFGDKEFLPQSAFLKW 242
QY 242 ASTKICNNKILWLCIEFMSLWAGSNKKNMNQRMDVYMSHAPTSSSVHNILHIKQLYHS 301
DB 243 LGTHVCTHVILKELCNLCFLCGFNERNLNMRDVTYTHSPAGTSVQNMLHWSQAVKF 302
QY 302 DEFRAVDGNDADNMKHYNQSHPPYIDLTAMKVPTAIWAGGHDVLTGTPDVARILPQIKS 361
DB 303 QKFOAFDWGSSAKNFHYNQSPPTYNVKDMLVPTAVWSGGHDWLDVYDVNILLTQITN 362
QY 362 LSLVLSLLPEWPTDFVWGLDAPQRMFSGNHL 395

Db 363 LVFHES-IPWE-HLDFIWLGLDAPWRLYNKIINL 394

RESULT 9

AA66061

ID AAB66061 standard; Protein; 399 AA.

AC AAB66061;

DT 30-MAR-2001 (first entry)

DE Human lysosomal acid lipase protein.

XX Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety.

OS Homo sapiens.

PN WO200077239-A2.

PD 21-DEC-2000.

PF 24-MAY-2000; 2000WO-US14858.

PR 14-JUN-1999; 99US-0333159.

PA (MILL-) MILLENNIUM PHARM INC.

XX McCarthy SA, Fraser CC, Sharp JD, Barnes TW;

PI WPI; 2001-032313/04.

DR TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's disease.

XX Claim 8; Fig.6; 359pp; English.

CC The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057, AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder. The present sequence is a sequence used in a sequence homology alignment with the TANGO/INTERCEPT sequences of the present invention.

XX Sequence 399 AA;

Query Match 51.1%; Score 1091; DB 22; Length 399;

Best Local Similarity 53.3%; Pred. No. 5.7e-101;

Matches 210; Conservative 63; Mismatches 119; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGTLNAGGFLDLNEVNPVWMTSEIIINYGPSEYEVTTEDGYILL 61

Db 3 MRFLGVVCLVLPWLPSESGGKUTAVDPETNMNVSEIIISYWGPPSEYLVETEDGYILC 62

Qy 62 VNRIPIYGRTHARSTGPRPVVYMOHALFADNAYVLENVAGFLGLADAGYDVWNGNSRG 121

Db 63 LNRIPGKKNHSDGKPPVFLQHLGLADSSNWTNLANSLGFLGLADAGFDVWNGNSRG 122

Qy 122 NTSRRHKTLSSETDEKFWAFSDEMAYDLPVDFIVNKTGOBKLYFIGHSLGTTIGFV 181

Db 123 NTSRRHKTLSVSDQEFWAFSDENAKYDLPASINFILNKTQEQVYVGHSGQTTIGFI 182

Qy 182 AFSTMPELAORIKMNFALGPTISFKYPTGIFTRFFELPNSIIKAVGTFKGFLEDKTKI 241

Db 183 AFSQIPELAKRIKMFALGPVAVAFCTSPMAKLGRLPDHLKDLFGDKEFLPQSAFLKW 242

Qy 242 ASTKICNNKILWLICSEFMSLWAGSNKKNMQSRDMVYMSHAPTSSVHNILHIKQLVHS 301

Db 243 LGTHVCTHVILKELCGNLCLFCFLGFGFERNLNSRDVYVTTTHSPAGTSVQNMLHWSQAVKF 302

Qy 302 DEFRAIDMGNDADNMKNHYNQSHPPYIDLTAMKVPTAIWAGGHVLTGTFODVARIILPQKS 361

Db 303 QKQAFDWGSSAKNYFHYNQSPPTNYVKMDLVPVAVMSGGHDWLDVYDVNILLTQITN 362

Qy 362 LSLVLSLLPEWEPTDFVWGLDAPORMFSGNHL 395

Db 363 LVFHES-IPWE-HLDFIWLGLDAPWRLYNKIINL 394

RESULT 10

AA660724

ID AAP60724 standard; Protein; 398 AA.

AC AAP60724;

DT 08-JUN-1991 (first entry)

DE Sequence of pregastric lipase.

XX Precursor polypeptide; secretion vector; enzyme.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= signal

XX Protein 20..398

PN WO8603778-A.

PD 03-JUL-1986.

XX 23-DEC-1985; 85WO-GB00599.

XX 21-DEC-1984; 84GB-0032483.

XX 23-DEC-1985; 85WO-GB00599.

XX 01-JAN-1986; 86GB-0019568.

XX (BREW-) BREWING RES FOUND.

PA (TUBB/) TUBB R S.

XX Tubb RS;

XX WPI; 1986-182910/28.

DR N-PSDB; AAN60685.

XX New precursor polypeptide of defined sequence - and corresp. DNA used to transform hosts for prodn. of the polypeptide

PT Example; Fig 5; 60pp; English.

PS The inventors claim a DNA sequence encoding AAP60723 linked to a promoter upstream and a gene for a polypeptide downstream.

CC Particular examples are the yeast enzyme AMG, the mammalian enzyme, gastric lipase and the mammalian lymphokine, interferon-alpha2.

XX Sequence 398 AA;

Query Match 49.2%; Score 1052; DB 7; Length 398;

Best Local Similarity 50.4%; Pred. No. 4.8e-97;

Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;

QY 2 MWLLTTTCLICGTLAGGFLDLENEVNPVWMTSEIIINYNGYPSEEVVTTEDGYILL 61
 Db 1 MWLLTMAISLVLTGTHGLFGLKHPGSPVWMTNISQIMITYWGYPNEEVETEDGYILE 60
 QY 62 VNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
 Db 61 VNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 120
 QY 122 NTSRRHKTLSSETDEKFWAFSPDEMAKYDLPVGVDFIVNKTGOEKLFFIGHSLGTTIGFV 181
 Db 121 NTWARRNLVSPDSVEFAFSPDEMAKYDLPATIDFIVKTKGQQLHYVGHSGTGTIGFI 180
 QY 182 AFSTMPELAQRIKMFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDDKTKI 241
 Db 181 AFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLRFVQSLFKFIFGDKIFYPHNFFDQF 240
 QY 242 ASTKICNNKILWLCSEFMSLWAGSNKKNNQSRMDVYVSHAPTSVSVNHLHIKOLYHS 301
 Db 241 LATEVCSREMLNLCSNALFIICGFDCKNFNTSRDLVYLSHNPAGTSVQNMFWHTQAVKS 300
 QY 302 DEFRAVDWGNADNMKHYNOSHPIIDLTAMKVPTAIWAGGHDVLGTPODVARILPOIKS 361
 Db 301 GKFOAYDWGSPVQNRMHYDOSPPYVNTAMNVPVIAVWNGKRDLLADPDQVGLLLPKLPN 360
 QY 362 LSLVLSLLPEWETFDVWGLDAPQRMFS 390
 Db 361 L-IYHKEIPFYN-HLDFIWAMDAPOEVYN 387

RESULT 11

AAW06058

ID AAP06058 standard; Protein; 398 AA.

AC AAW06058;

DT 22-AUG-1991 (first entry)

XX Sequence of human pregastric lipase.

DE Cystic fibrosis therapy; enzyme; lipase deficiency.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein 20..398

XX W08601532-A.

XX 13-MAR-1986.

XX 15-AUG-1985; 85WO-GB00364.

XX 21-AUG-1984; 84GB-0021210.

PR 15-AUG-1985; 85WO-GB00364.

PR 01-JAN-1986; 86GB-0008897.

XX (CELL-) CELYTECH LTD.

PA (LOWE/) LOWE P A.

XX Lowe PA;

DR WPI; 1986-081634/12.

DR N-PSDB; AAN60566.

XX New gastric lipase protein, esp. of human origin - for treating

PT lipase deficiency, and DNA sequences coding for it

XX Disclosure; Fig 3; 39pp; English.

XX The inventors claim a pregastric lipase protein and a gene encoding

CC it. Gastric lipase protein is useful for oral administration to

CC treat lipase deficiency, e.g. cystic fibrosis or pancreatitis.

XX SQ Sequence 398 AA;
 Query Match 49.2%; Score 1052; DB 7; Length 398;
 Best Local Similarity 50.4%; Pred. No. 4.8e-97;
 Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;
 QY 2 MWLLTTTCLICGTLAGGFLDLENEVNPVWMTSEIIINYNGYPSEEVVTTEDGYILL 61
 Db 1 MWLLTMAISLVLTGTHGLFGLKHPGSPVWMTNISQIMITYWGYPNEEVETEDGYILE 60
 QY 62 VNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
 Db 61 VNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 120
 QY 122 NTSRRHKTLSSETDEKFWAFSPDEMAKYDLPVGVDFIVNKTGOEKLFFIGHSLGTTIGFV 181
 Db 121 NTWARRNLVSPDSVEFAFSPDEMAKYDLPATIDFIVKTKGQQLHYVGHSGTGTIGFI 180
 QY 182 AFSTMPELAQRIKMFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDDKTKI 241
 Db 181 AFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLRFVQSLFKFIFGDKIFYPHNFFDQF 240
 QY 242 ASTKICNNKILWLCSEFMSLWAGSNKKNNQSRMDVYVSHAPTSVSVNHLHIKOLYHS 301
 Db 241 LATEVCSREMLNLCSNALFIICGFDCKNFNTSRDLVYLSHNPAGTSVQNMFWHTQAVKS 300
 QY 302 DEFRAVDWGNADNMKHYNOSHPIIDLTAMKVPTAIWAGGHDVLGTPODVARILPOIKS 361
 Db 301 GKFOAYDWGSPVQNRMHYDOSPPYVNTAMNVPVIAVWNGKRDLLADPDQVGLLLPKLPN 360
 QY 362 LSLVLSLLPEWETFDVWGLDAPQRMFS 390
 Db 361 L-IYHKEIPFYN-HLDFIWAMDAPOEVYN 387

RESULT 12

AAW09383

ID AAW09383 standard; Protein; 398 AA.

AC AAW09383;

DT 19-AUG-1997 (first entry)

XX Human gastric lipase protein sequence.

DE Duodenal; gastric; lipase; transgenic; plant; recombinant; extract;

XX food; absorption; fat; pancreatic; cystic fibrosis; exocrine; dairy;

XX hydrolysis; trans-esterification; substrate; enzyme; biofuel; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /note= "signal peptide"

FT Protein /note= "mature protein"

XX W09633277-A2.

XX 24-OCT-1996.

XX 19-APR-1996; 96WO-FR00606.

XX 20-APR-1995; 95FR-0004754.

XX (BIOC-) BIOCEM SA.

PA (LJOU) INST RECH JOUVEINAL.

XX Baudino S, Benicourt C, Cudrey C, Gruber V, Lenee P;

XX Merot B;

XX WPI; 1996-485783/48.

DR N-PSDB; AAT58916.
 XX Recombinant human or canine pre-duodenal lipase prodn. in transgenic
 PT plants - useful for facilitating absorption of fat, as bio-catalysts
 PT and for prodn. of bio-fuel
 XX
 XX Claim 3; Fig 5; 130pp; French.
 XX
 CC This is the amino acid sequence of the human pre-duodenal (i.e. gastric)
 CC lipase enzyme. The sequence can be used to generate transgenic plants
 CC producing recombinant lipase in an enzymatically active form.
 CC Alternatively amino acids 20-23 or 20-73 (1-4 or 1-54 of the mature
 CC protein, respectively) can be deleted to form the derivatives designated
 CC delta-4 or delta-54 respectively. Plants, or their extracts, expressing
 CC the lipases or the truncated derivatives, can be used:
 CC (a) as pharmaceuticals or food to facilitate absorption of fat, either
 CC in healthy subjects or in patients with inadequate levels of
 CC gastric/pancreatic lipase e.g. those with cystic fibrosis or exocrine
 CC pancreatic insufficiency, in the elderly or in patients undergoing medical
 CC treatment which alters fat adsorption; (b) for performing industrial or
 CC agricultural reactions, e.g. in processing of fats or in the dairy
 CC industry, for hydrolysis or transesterification reactions, etc., where
 CC the plant material may provide both enzyme and substrate. The transgenic
 CC plants can also be used for biofuel production.
 XX
 SQ Sequence 398 AA;
 Query Match 49.2%; Score 1052; DB 17; Length 398;
 Best Local Similarity 50.4%; Pred. No. 4.8e-97;
 Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;
 Qy 2 MWLLTTTCLICGTNLNAGGFLDLENEVNPVMMNTSEIIYNGPSEYEVTTEDGYILL 61
 Db 1 MWLLTMSALISVLGTTGFLGKLPSPVMTNISQMTYWGYPNEEVVTDGYILE 60
 Qy 62 VNRIPYGRTHARSTGPRPVYVMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
 Db 61 VNRIPYGRKNSGNTGQRPVFLQHGLLASATNWTISNLPNNSLAFTLADAGYDVMGNSRG 120
 Qy 122 NTSRRHKTLSITDCKFWAFSFDENAKYDLPVDFVYKTKGOEKLFIHSGTIGFV 181
 Db 121 NTSRRHKTLSITDCKFWAFSFDENAKYDLPVDFVYKTKGOEKLFIHSGTIGFV 180
 Qy 182 AFSTMPQLAQRKMFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKFLEDKTKI 241
 Db 181 AFSTNPLSAKRITKTYALAPVATVTKYTKSLINKLRFVPSLKFIFGDKIFVPHNFFDQF 240
 Qy 242 ASTKICNNKILWLCSEFWSLWAGSNKKNQSMQSDVYMSHAPTSSVHNILHIKQLYHS 301
 Db 241 LATEVCSREMLNLLCSNALFTICGDFSKNFNTSRDLYVLSHNPAGTSVQNNMFHWTQAVKS 300
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 Qy 362 LSLVLSLLPEWEPTDFVWGLDAPQRMFS 390
 Db 361 L-IYHKEIPFYN-HLDFIWDAPQEVYN 387
 RESULT 13
 AAB66086
 ID AAB66086 standard; protein; 398 AA.
 AC AAB66086;
 XX
 XX 30-MAR-2001 (first entry)
 DT Human lipase protein.
 XX
 DE Gene therapy: TANGO protein; INTERCEPT protein; neurological disorder;
 KW central nervous system; focal brain disorder; bipolar affective disorder;
 KW global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;

KW senile dementia; Huntington's disease; amyotrophic lateral sclerosis;
 KW Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;
 KW neuropsychiatric; psychoactive substance use; anxiety.
 OS Homo sapiens.
 XX
 XX WO2000077239-A2.
 PN
 XX 21-DEC-2000.
 PD
 XX 24-MAY-2000; 2000WO-US14858.
 PF
 XX 14-JUN-1999; 99US-0333159.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX McCarthy SA, Fraser CC, Sharp JD, Barnes TM;
 PI WPI; 2001-032313/04.
 XX
 XX TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for
 XX screening assays and diagnostic assays and for the treatment of
 PT neurological diseases such as Alzheimer's, Parkinson's and Huntington's
 PT disease -
 PT
 XX
 XX Disclosure; Fig 6; 359pp; English.
 PS
 XX The present invention relates to TANGO or INTERCEPT proteins and coding
 CC sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057,
 CC AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding
 CC sequences are useful for the treatment of neurological disorders such as
 CC central nervous system (CNS) disorders, CNS-related disorders, focal
 CC brain disorders, global-diffuse cerebral disorders and other
 CC neurological and cerebrovascular disorders. The CNS disorders include
 CC Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic
 CC lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome,
 CC autonomic function disorders such as hypertension and sleep disorders,
 CC neuropsychiatric disorders, psychoactive substance use disorders,
 CC anxiety, and bipolar affective disorder. The present sequence is a
 CC sequence used in a sequence homology alignment with the TANGO/INTERCEPT
 CC sequences of the present invention.
 XX
 SQ Sequence 398 AA;
 Query Match 49.2%; Score 1052; DB 22; Length 398;
 Best Local Similarity 50.4%; Pred. No. 4.8e-97;
 Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;
 Qy 2 MWLLTTTCLICGTNLNAGGFLDLENEVNPVMMNTSEIIYNGPSEYEVTTEDGYILL 61
 Db 1 MWLLTMSALISVLGTTGFLGKLPSPVMTNISQMTYWGYPNEEVVTDGYILE 60
 Qy 62 VNRIPYGRTHARSTGPRPVYVMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
 Db 61 VNRIPYGRKNSGNTGQRPVFLQHGLLASATNWTISNLPNNSLAFTLADAGYDVMGNSRG 120
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 Db 121 NTSRRHKTLSITDCKFWAFSFDENAKYDLPVDFVYKTKGOEKLFIHSGTIGFV 180
 Qy 182 AFSTMPQLAQRKMFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKFLEDKTKI 241
 Db 181 AFSTNPLSAKRITKTYALAPVATVTKYTKSLINKLRFVPSLKFIFGDKIFVPHNFFDQF 240
 Qy 242 ASTKICNNKILWLCSEFWSLWAGSNKKNQSMQSDVYMSHAPTSSVHNILHIKQLYHS 301
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 Db 301 GKFOAYDNGSPVQNRHMDQSQPPYNYVTAMNVPYAVWNGKDLADQDVGLLLPKLPN 360
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| : : | : | : | : | : | :
361 L-IYHKEIPFYN-HLDFIWAMDAPOEYVN 387
Db

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RESULT 14

AAE11931
ID AAE11931 standard; Protein; 409 AA.

XX
AC AA E11931;

XX
DT 18-DEC-2001 (first entry)

XX
DE Human CG162 (or C59) lipase protein #2.

xx Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina;
 xx cardiovascular disease; lipid metabolism; myocardial infarction;
 kw cerebral ischaemia; arterial thrombosis; thrombolytic; antilipemic;
 kw coronary artery thrombosis; cerebral artery thrombosis; stroke;
 kw intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
 kw neuroprotectant; cerebroprotective.

XX Homo sapiens.

XX	FH	Key	Location/Qualifiers

FT	key	Local
FT	Peptide	1..19

	/label=	signal_peptide
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FT	Protein	20..409
FT	Protein	20..409

/note= "Human mature CG162 (or C59) lipase protein"

PN WO200179446-A2.

25-OCT-2001.

XX 16-APR-2001; 2001WO-US12529.
PF

XX
PR 14-APR-2000; 2000US-197137P.

PR 14-APR-2000; 2000US-197137P.
PR 20-JUN-2000; 2000US-0598042.

PR 20-JUN-2000; 2000US-0398042.
PR 03-AUG-2000; 2000US-0631451.

PR 22-SEP-2000; 2000US-0667298.

PR 17-NOV-2000; 2000US-0714936.

PA (HYSE-) HYSEQ INC.

PI Ballinger DG, Loeb D, Montgomery JR, Tang TY, Zhou P, Goodrich R;

PI Liu C, Asundi V, Zhao QA, Wehrman T, Drmanac RT, Ren F, Qian XB;

PI Wang D;

DR WPI; 2001-611724/70.

DR N-PSDB; AAD19226.

PT Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein
PT receptor polypeptides, useful for preventing diagnosing and treating
PT lipid metabolism disorders, thrombosis and cardiovascular diseases -

PS Claim 10; Fig 3; 266pp; English.

The invention relates to polynucleotides encoding proteins CG122, CG179, CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins involved in lipid metabolism and cardiovascular disease such as human apolipoproteins, lipases and lipoprotein receptor proteins. These DNA and protein sequences are useful for treating or preventing disorders associated with apolipoproteins, lipases and lipoprotein receptor (ALLr) expression and for treating lipid metabolism, cardiovascular diseases and thrombosis. Antibodies against these proteins are useful for determining the presence of or predisposition to a disease associated with altered levels of these sequences. ALLr polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them and cells expressing ALLr proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of this polypeptide. Vectors comprising these DNA and protein sequences are also useful for producing ALLr proteins. The nucleic acids and polypeptides of the invention are also useful for the treatment of occlusive cardiovascular

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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:34:17 ; Search time 19 seconds
(without alignments)
1270.986 Million cell updates/sec

Title: US-10-003-302-2

Perfect score: 2137

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Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2137	100.0	395	12	US-10-003-302-2
2	2030	95.0	398	9	US-10-056-744B-2
3	1097	51.3	392	12	US-10-003-302-4
4	1091	51.1	399	9	US-10-042-431-41
5	1091	51.1	399	9	US-09-759-130B-411
6	1052	49.2	398	9	US-10-042-431-75
7	1052	49.2	398	9	US-09-759-130B-445
8	1031	48.2	409	10	US-09-835-996A-21
9	1031	48.2	423	9	US-10-042-431-47
10	1031	48.2	423	9	US-09-759-130B-417
11	1023	47.9	390	9	US-10-042-431-49
12	1023	47.9	390	9	US-09-759-130B-419
13	995	46.6	374	10	US-09-811-825-4
14	995	46.6	398	10	US-09-811-825-2
15	700	32.8	221	9	US-10-042-431-50
16	700	32.8	221	9	US-09-759-130B-420
17	341	16.0	127	9	US-10-056-744B-5
18	297	13.9	144	9	US-10-042-431-52
19	297	13.9	144	9	US-09-759-130B-422

20	111	5.2	297	12	US-10-080-644-7	Sequence 7, Appli
21	96	4.5	262	9	US-10-027-800-35	Sequence 35, Appl
22	96	4.5	262	9	US-10-027-800-35	Sequence 35, Appl
23	96	4.5	262	10	US-09-903-410-35	Sequence 35, Appl
24	94.5	4.4	305	10	US-09-815-242-12337	Sequence 12337, A
25	90.5	4.2	222	10	US-09-815-242-5276	Sequence 5276, Ap
26	90	4.2	286	10	US-09-950-368-9	Sequence 9, Appli
27	89.5	4.2	494	9	US-10-066-500-139	Sequence 139, App
28	89.5	4.2	494	9	US-10-066-796-139	Sequence 139, App
29	89.5	4.2	494	9	US-10-066-273-139	Sequence 139, App
30	89.5	4.2	494	9	US-10-066-494-139	Sequence 139, App
31	89.5	4.2	494	9	US-10-066-269-139	Sequence 139, App
32	89.5	4.2	494	9	US-10-066-193-139	Sequence 139, App
33	89.5	4.2	494	9	US-10-066-211-139	Sequence 139, App
34	89	4.2	297	9	US-10-027-805-37	Sequence 37, Appl
35	89	4.2	297	9	US-10-027-804-37	Sequence 37, Appl
36	89	4.2	297	10	US-09-903-410-37	Sequence 37, Appl
37	87.5	4.1	480	10	US-09-881-752A-38	Sequence 38, Appl
38	86.5	4.0	341	10	US-09-799-777-61	Sequence 61, Appl
39	86.5	4.0	441	10	US-09-729-402-8	Sequence 8, Appli
40	86.5	4.0	564	9	US-09-944-160-12	Sequence 12, Appl
41	86	4.0	1183	9	US-09-870-759-45	Sequence 45, Appl
42	85	4.0	678	9	US-09-738-626-6025	Sequence 6025, Ap
43	84.5	4.0	770	9	US-09-992-896-9	Sequence 9, Appli
44	83.5	3.9	770	10	US-09-815-656-31	Sequence 31, Appl
45	83	3.9	719	9	US-10-234-266-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-003-302-2
; Sequence 2, Application US/10003302
; Patent No. US20020142435A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01186DIV
; CURRENT APPLICATION NUMBER: US/10/003.302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-302-2

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Best Local Similarity	100.0%	Pred. No.	1.6e-204;				
Matches	395;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MMWLLTTTCLICGTLNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTTEDGYL	60				
Oy	61	LVNRIPTYGRTHARSTGPRPVVYMQHALFADNAYWLENANGSLGFLADAGYDVMGNSR	120				
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Db	121	GNTWSRRKTLTSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTIGF	180				
Oy	181	VAFTMPLEAORIKMNFALGPTISFKYPTGIFTRFLLPNSTIKAVFGTKGFLEDDKTK	240				
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Db	241	IATKICNKNILWLITCSFMSLWAGSNKNNQSMQMDVYMSHAPTGSVVHNTLHKQLYH	300				

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Db 361 SLSVLSSLPEWEPTDFVWGLDAPQRMFSGNHL 395
RESULT 2
US-10-056-744B-2
; Sequence 2, Application US/10056744B
; Publication No. US20020193303A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL ESTER
; FILE OF INVENTION: HYDROLASE AND USES THEREFOR
; FILE REFERENCE: MPI2001-026PIRNM
; CURRENT APPLICATION NUMBER: US/10/056,744B
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/264,167
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-744B-2
Query Match 95.0%; Score 2030; DB 9; Length 398;
Best Local Similarity 97.2%; Pred. No. 7.1e-194;
Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;
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Db 61 LVNRIPIYGRTHARSTGPRPVVYMOHALFADNAYWLENANGSLGFLADAGYDVMWGNRS 120
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RESULT 3
US-10-003-302-4
; Sequence 4, Application US/10003302
; Patent No. US20020142435A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01186DIV
; CURRENT APPLICATION NUMBER: US/10/003,302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-302-4
Query Match 51.3%; Score 1097; DB 12; Length 392;
Best Local Similarity 53.6%; Pred. No. 5.5e-107;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;
Qy 2 MWLLLTTCICGTLNAGGFLDLENEVPEVMMNTSEIIINYGPSEYEYVTTEDGYILL 61
Db 1 MRFLGLVVLVLTWLHSESGGKLTAVDPTNMNYSIIISYWGFPSEYLVETEDGYILC 60
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Db 61 LNRIPHGRKNHSDKGPVVFLOHGLLADSSNNVVTNLANSSLGFLADAGFDVWGNRS 120
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RESULT 4
US-10-042-431-41
; Sequence 41, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; FILE REFERENCE: 10147-602
; CURRENT APPLICATION NUMBER: US/10/042,431
; PRIOR FILING DATE: 2001-10-25
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
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Db 243 LGTHVCTHVILKELCGNLCFLCGFNERNLNNSRDVYVTHSPAGTSVQNMLHWSQAVKF 302
Qy 302 DEFRAIDMGNDADNMKNHYNOSHPPIYDLTAMKVPYTAIWAGGHDVLTGTPQDVARIILPOIKS 361
Db 303 QKQAFDVGSSAKNFYHNSYPTPYNVKMDLVPYAVWSSGGHDLADYVDVNWILLTQITN 362
Qy 362 LSLVLSLLPEWPTDFVWGLDAPQRMFSGHNHL 395
Db 363 LVFHES-IPWE-HLDFIWLGLDAPWRLYNKIINL 394

RESULT 5
US-09-759-1308-411
; Sequence 411, Application US/097591308
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-5350MNI
; CURRENT APPLICATION NUMBER: US/09759,1308
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
```

```
Query Match 51.1%; Score 1091; DB 9; Length 399;
Best Local Similarity 53.3%; Pred. No. 2.2e-100;
Matches 210; Conservative 63; Mismatches 119; Indels 2; Gaps 2;
Qy 2 MWLLTTTCLTCGTLNAGGFLDLENEVNPVMMNTSEIIYNGYPSSEYEVETEDGYILL 61
Db 3 MRFLGLVCLVLPWHLSESGGKLTAVDPETNMNVEIISYWGFFSEYLVETEDGYILC 62
Qy 62 VNRIPIYGRTHARSTGPRPVYVYMHQALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 63 LNRIPHGRKNSHSDKPKPVFLQHLGLLADSSNWNVTNLANSLSGLFLADAGFDVWNGNSRG 122
Qy 122 NTWSRHHKTLSETDEKFWAFSDENAKYDLPQVIDFVYVNTGOEKLIFIGHSLGTTIGFV 181
Db 123 NTWSRHHKTLVSQDEFWAFSDENAKYDLPASINFILNKTGQEQVYVYVHSGQTTIGFI 182
Qy 182 AFSTMPELAQRIKMFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 183 AFSQIPELAKRIKMFALGPVAVAFCTSPMAKLGRLDPHLIKDLFGDKEFLPQSAFLKW 242
Qy 242 ASTKICNNKILWICSEFMSLWAGSNKKNMOSRDVYVMSHAPTSSVHNILHIKQLYHS 301
Db 243 LGTHVCTHVILKELCGNLCFLCGFNERNLNNSRDVYVTHSPAGTSVQNMLHWSQAVKF 302
Qy 302 DEFRAIDMGNDADNMKNHYNOSHPPIYDLTAMKVPYTAIWAGGHDVLTGTPQDVARIILPOIKS 361
Db 303 QKQAFDVGSSAKNFYHNSYPTPYNVKMDLVPYAVWSSGGHDLADYVDVNWILLTQITN 362
Qy 362 LSLVLSLLPEWPTDFVWGLDAPQRMFSGHNHL 395
Db 363 LVFHES-IPWE-HLDFIWLGLDAPWRLYNKIINL 394

RESULT 6
US-10-042-431-75
; Sequence 75, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-602
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-431-75

Query Match 49.2%; Score 1052; DB 9; Length 398;
Best Local Similarity 50.4%; Pred. No. 1.7e-96;
Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;
Qy 2 MWLLTTTCLTCGTLNAGGFLDLENEVNPVMMNTSEIIYNGYPSSEYEVETEDGYILL 61
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Db 1 MWLLLTMASLISVLGTHGLFKLHGPSPEVTMNISQMITWGYPNEEYEVVTEGYLE 60
QY 62 VNRIPIGRTHARSTGRPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 61 VNRIPIGKKNNGTGRPVVFLQHLASATWISNLPNNSLAFILADAGYDVWNGNSRG 120
QY 122 NTSRRHKTLSDETKFWAFSDEMAKYDLPVDFIVNKTQOEKLYFIGHSLGTTIGFV 181
Db 121 NTSRRHKTLSDETKFWAFSDEMAKYDLPVDFIVNKTQOEKLYFIGHSLGTTIGFV 180
QY 182 AFTMPQLAQRKMKMFLGPTISFKYPTGIFTRFELLNSIIKAVGTFKGFLEDDKTKI 241
Db 181 AFTMPQLAQRKMKMFLGPTISFKYPTGIFTRFELLNSIIKAVGTFKGFLEDDKTKI 240
QY 242 ASTKICNNKILWLCSEFMSLWAGSNKKNMOSRMDVYMSHAPTSSVHNILHIKQLYHS 301
Db 241 LATEVCSREMLNLLCSNALFIICGFSKFNFTSRDLVLSHNPAGTSVONMFHTQAVKS 300
QY 302 DEFAYDNGNDANMKHYNQSHPPYIDLTAMKVPTAIWAGGHVLTGTPQDVARILPQIKS 361
Db 301 GKFOAYDWGSPVQNRMHYDQSPPYVNTAMNVPVAVWNGGKDLLADPDVGLLLPKLPN 360
QY 362 LSLVLSLLPEWEPTDFVWGLDAPQRMES 390
Db 361 L-IYHKEIPFYN-HLDFIWAMDAPQEVYN 387
```

RESULT 7

```
US-09-759-130B-445
; Sequence 445, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 445
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-445

Query Match 49.2%; Score 1052; DB 9; Length 398;
Best Local Similarity 50.4%; Pred. No. 1.7e-96;
Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;

QY 2 MWLLLTTCCTGCTNAGSFLDLENVNPEVMMNTSEIIYNGYPSSEEVVTEGYLE 61
Db 1 MWLLLTMASLISVLGTHGLFKLHGPSPEVTMNISQMITWGYPNEEYEVVTEGYLE 60
QY 62 VNRIPIGRTHARSTGRPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 61 VNRIPIGKKNNGTGRPVVFLQHLASATWISNLPNNSLAFILADAGYDVWNGNSRG 120
QY 122 NTSRRHKTLSDETKFWAFSDEMAKYDLPVDFIVNKTQOEKLYFIGHSLGTTIGFV 181
Db 121 NTSRRHKTLSDETKFWAFSDEMAKYDLPVDFIVNKTQOEKLYFIGHSLGTTIGFV 180
QY 182 AFTMPQLAQRKMKMFLGPTISFKYPTGIFTRFELLNSIIKAVGTFKGFLEDDKTKI 241
Db 181 AFTMPQLAQRKMKMFLGPTISFKYPTGIFTRFELLNSIIKAVGTFKGFLEDDKTKI 240
QY 242 ASTKICNNKILWLCSEFMSLWAGSNKKNMOSRMDVYMSHAPTSSVHNILHIKQLYHS 301
Db 241 LATEVCSREMLNLLCSNALFIICGFSKFNFTSRDLVLSHNPAGTSVONMFHTQAVKS 300
QY 302 DEFAYDNGNDANMKHYNQSHPPYIDLTAMKVPTAIWAGGHVLTGTPQDVARILPQIKS 361
Db 301 GKFOAYDWGSPVQNRMHYDQSPPYVNTAMNVPVAVWNGGKDLLADPDVGLLLPKLPN 360
QY 362 LSLVLSLLPEWEPTDFVWGLDAPQRMES 390
Db 361 L-IYHKEIPFYN-HLDFIWAMDAPQEVYN 387

RESULT 8
US-09-835-996A-21
; Sequence 21, Application US/09835996A
; Patent No. US20020142953A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis
; APPLICANT: Loeb, Debra
; APPLICANT: Montgomery, Julie
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qing
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje
; APPLICANT: Ren, Feiyan
; APPLICANT: Qian, Xiaohong
; APPLICANT: Wang, Dunrui
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
; FILE REFERENCE: 28110/35915A
; CURRENT APPLICATION NUMBER: US/09/835,996A
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/197,137
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/714,936
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/667,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
```


SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 409
TYPE: PRT
ORGANISM: Homo sapiens
US-09-835-996A-21

Query Match 48.2%; Score 1031; DB 10; Length 409;
Best Local Similarity 51.0%; Pred. No. 2.2e-94;
Matches 199; Conservative 61; Mismatches 124; Indels 6; Gaps 4;

```
QY 2 MWLLTTTCLICGILNACGFLDLENE-VNPEVWMTSEIIYNGVPSEYEVTTEDGYIL 60
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 3 MWLLILVAYMFQFNVNS---VHMPTKAVDPEAFNMISIIHQGYPCPEYEVATEDGYIL 59
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 61 LVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVWNGNSR 120
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 60 SVNRIPRGLVQPKTGSRPVLLQHLGVLGGASNWNISLNNPNSLGLFADAGFDVWNGNSR 119
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 121 GNTWSRRHKTSETDEKFWAFSDFEMAKYDLPVGVIDFIVNKTGQEKLYFIGHSLGTTIGF 180
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 120 GNWSRKHKTLSIDQDEFWAFSYDEMAREFDLPVINFILQKTGQEKIYVVGYSQGTTFMGF 179
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 181 VAFSTMPLELAQRIKKNFALGPTISFKYPTGIFTRFLLPNSLIKAVFGTKGFFLEDKTK 240
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 180 IAFSTMPLELAQRIKKNFALGPTISFKYPTGIFTRFLLPNSLIKAVFGTKGFFLEDKTK 240
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 241 IASTKICNNKILWLICSEFMSLWAGSNKKNMOSRMDVYMSHAPTGVSSVHNILHIKOLYH 300
   :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 240 QLVYLCQVILDQICSNIMLLGGFNTNNMNSRASVYAHTLAGTSVQNLHWSQAVN 299
   :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 301 SDEFRAYDNGDADNMKNHYNOSHPIYDLTAMKVPTAIWAGGHVILGTPQDVVARILPQIK 360
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 300 SGELRAFDSGSETKLEKCNQPTPVRYRVDRMTVPTAMWTGGQDWLSNPEDVKMLLSEVT 359
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 361 SLSLVLSLLPEWPTFFDFVWGLDAPQRMFS 390
   :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 360 NL-IYHKNIPWAHV-DFIWGLDAPHRMYN 387
   :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
```

RESULT 9

US-10-042-431-47
Sequence 47, Application US/10042431
Publication No. US20020182675A1
GENERAL INFORMATION:
APPLICANT: MCCARTHY, Sean A
APPLICANT: BARNES, Thomas M
APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-6U2
CURRENT APPLICATION NUMBER: US/10/042,431
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 423
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-431-47

Query Match 48.2%; Score 1031; DB 9; Length 423;
Best Local Similarity 51.0%; Pred. No. 2.3e-94;
Matches 199; Conservative 61; Mismatches 124; Indels 6; Gaps 4;

```
QY 2 MWLLTTTCLICGILNACGFLDLENE-VNPEVWMTSEIIYNGVPSEYEVTTEDGYIL 60
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 17 MWLLILVAYMFQFNVNS---VHMPTKAVDPEAFNMISIIHQGYPCPEYEVATEDGYIL 73
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
```

```
QY 61 LVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVWNGNSR 120
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 74 SVNRIPRGLVQPKTGSRPVLLQHLGVLGGASNWNISLNNPNSLGLFADAGFDVWNGNSR 133
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 121 GNTWSRRHKTSETDEKFWAFSDFEMAKYDLPVGVIDFIVNKTGQEKLYFIGHSLGTTIGF 180
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 134 GNWSRKHKTLSIDQDEFWAFSYDEMAREFDLPVINFILQKTGQEKIYVVGYSQGTTFMGF 193
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 181 VAFSTMPLELAQRIKKNFALGPTISFKYPTGIFTRFLLPNSLIKAVFGTKGFFLEDKTK 240
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 194 IAFSTMPLELAQRIKKNFALGPTISFKYPTGIFTRFLLPNSLIKAVFGTKGFFLEDKTK 253
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 241 IASTKICNNKILWLICSEFMSLWAGSNKKNMOSRMDVYMSHAPTGVSSVHNILHIKOLYH 300
   :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 254 QLVYLCQVILDQICSNIMLLGGFNTNNMNSRASVYAHTLAGTSVQNLHWSQAVN 313
   :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 301 SDEFRAYDNGDADNMKNHYNOSHPIYDLTAMKVPTAIWAGGHVILGTPQDVVARILPQIK 360
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 314 SGELRAFDSGSETKLEKCNQPTPVRYRVDRMTVPTAMWTGGQDWLSNPEDVKMLLSEVT 373
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 361 SLSLVLSLLPEWPTFFDFVWGLDAPQRMFS 390
   :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 374 NL-IYHKNIPWAHV-DFIWGLDAPHRMYN 401
   :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
```

RESULT 10

US-09-759-130B-417
Sequence 417, Application US/09759130B
Publication No. US20030022279A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirst, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES
FILE REFERENCE: MPI00-5350MIM
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 417
LENGTH: 423


```
Query Match 47.9%; Score 1023; DB 9; Length 390;
Best Local Similarity 53.4%; Pred. No. 1.3e-93;
Matches 194; Conservative 54; Mismatches 113; Indels 2; Gaps 2;

Qy 28 VNPVWMTSEIIYNGYPSSEYEVTEDGYILLVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLE 87
Db 8 VDPEAFMNLSEIIHQGYPCSEYEVEDGYILSVNRIPRGLVQPKTGSRPVVLQHL 67

Qy 88 FADNAYWLENTANGSLGFLLDAGYDVWNGSRGNTWRRHKTSETDEKFWAFSDMA 147
Db 68 VCGASNLISLNPNSLGFILADAGFDVWNGSRGNARSKHKTLSIDQDEFWAFSDMA 127

Qy 148 KYDLPVDFIVNKTGQKLYFIHSLGTTIGFVAFSTMPPELAQRKMFALGPTISPKY 207
Db 128 RFDLPVDFIVNKTGQKLYFIHSLGTTIGFVAFSTMPPELAQRKMFALGPTISPKY 187

Qy 208 PTGIFTRFLLPNSIIKAVGTFKFFLEDKTKTASTKICNNKILWLCSEFMSLWAGSN 267
Db 188 AKSPGTFKFLPDMMIKGLFKKFLYQTRFLQVILYLCGVILQDQICSNIMLLGGFN 247

Qy 268 KKNMOSRMDVMSHAPTSSVHNILHIKOLYHSDFRAYDWGNDADNMKHYNQSHPPY 327
Db 248 TNNMNSRASVYAAHTLAGTSVQNLHWSQAVNSGELRAFDWGSSEKLEKCNQPTPVRY 307

Qy 328 DLTAMKVPATWAGHDVLTGPQDVARILPOIKSLSLVLSLLPEWEPFTDFVWGLDAPOR 387
Db 308 RVRDMTPTAMWTGGQWLSNPEDVKMLLSEVTNL-IYHKNIPWAHV-DFIWGLDAPHRMYN 365

Qy 388 MFS 390
Db 366 MIN 368

RESULT 13
US-09-811-825-4
; Sequence 4, Application US/09811825
; Patent No. US20020144297A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; FILE REFERENCE: CL001170
; CURRENT APPLICATION NUMBER: US/09/811.825
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Human
US-09-811-825-4

Query Match 46.6%; Score 995; DB 10; Length 374;
Best Local Similarity 53.4%; Pred. No. 7.4e-91;
Matches 189; Conservative 52; Mismatches 111; Indels 2; Gaps 2;

Qy 37 SEIIYNGYPSSEYEVTEDGYILLVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLE 96
Db 1 SEIIHQGYPCSEYEVEDGYILSVNRIPRGLVQPKTGSRPVVLQHLGVLGGASNMIS 60

Qy 97 NYANGSLGFLLDAGYDVWNGSRGNTWRRHKTSETDEKFWAFSDMAKYDLPGVID 156
Db 61 NLPNNSLGFILADAGFDVWNGSRGNARSKHKTLSIDQDEFWAFSDMAKFDLPVAVIN 120

Qy 157 FIVNKTGQKLYFIHSLGTTIGFVAFSTMPPELAQRKMFALGPTISFKYPTGIFTRFF 216
Db 121 FILQKTGQEKIYVYVSGQTTMGFTAFSTMPPELAQIKMYFALPATVKKHAKSPGTFKL 180

Qy 217 LLPNSIIKAVGTFKFFLEDKTKTASTKICNNKILWLCSEFMSLWAGSNKKNQSRM 276
Db 181 LLPDMMIKGLFKKFLYQTRFLQVILYLCGVILQDQICSNIMLLGGFNTNNMNSRA 240

RESULT 15
US-10-042-431-50
; Sequence 50, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-602
; CURRENT APPLICATION NUMBER: US/10/042.431
; CURRENT FILING DATE: 2001-10-25
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Qy 277 DVYMSHAPTSSVHNILHIKOLYHSDFRAYDWGNDADNMKHYNQSHPPYDLTAMKVPT 336
Db 241 SVYAAHTLAGTSVQNLHWSQAVNSGELRAFDWGSSEKLEKCNQPTPVRYRVRDMTVP 300

Qy 337 AIWAGHDVLTGPQDVARILPOIKSLSLVLSLLPEWEPFTDFVWGLDAPQRMFS 390
Db 301 AMWTGGQWLSNPEDVKMLLSEVTNL-IYHKNIPWAHV-DFIWGLDAPHRMYN 352

RESULT 14
US-09-811-825-2
; Sequence 2, Application US/09811825
; Patent No. US20020144297A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; FILE REFERENCE: CL001170
; CURRENT APPLICATION NUMBER: US/09/811.825
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Human
US-09-811-825-2

Query Match 46.6%; Score 995; DB 10; Length 398;
Best Local Similarity 53.4%; Pred. No. 8.1e-91;
Matches 189; Conservative 52; Mismatches 111; Indels 2; Gaps 2;

Qy 37 SEIIYNGYPSSEYEVTEDGYILLVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLE 96
Db 25 SEIIHQGYPCSEYEVEDGYILSVNRIPRGLVQPKTGSRPVVLQHLGVLGGASNMIS 84

Qy 97 NYANGSLGFLLDAGYDVWNGSRGNTWRRHKTSETDEKFWAFSDMAKYDLPGVID 156
Db 85 NLPNNSLGFILADAGFDVWNGSRGNARSKHKTLSIDQDEFWAFSDMAKFDLPVAVIN 144

Qy 157 FIVNKTGQKLYFIHSLGTTIGFVAFSTMPPELAQRKMFALGPTISFKYPTGIFTRFF 216
Db 145 FILQKTGQEKIYVYVSGQTTMGFTAFSTMPPELAQIKMYFALPATVKKHAKSPGTFKL 204

Qy 217 LLPNSIIKAVGTFKFFLEDKTKTASTKICNNKILWLCSEFMSLWAGSNKKNQSRM 276
Db 205 LLPDMMIKGLFKKFLYQTRFLQVILYLCGVILQDQICSNIMLLGGFNTNNMNSRA 264

Qy 277 DVYMSHAPTSSVHNILHIKOLYHSDFRAYDWGNDADNMKHYNQSHPPYDLTAMKVPT 336
Db 265 SVYAAHTLAGTSVQNLHWSQAVNSGELRAFDWGSSEKLEKCNQPTPVRYRVRDMTVP 324

Qy 337 AIWAGHDVLTGPQDVARILPOIKSLSLVLSLLPEWEPFTDFVWGLDAPQRMFS 390
Db 325 AMWTGGQWLSNPEDVKMLLSEVTNL-IYHKNIPWAHV-DFIWGLDAPHRMYN 376

RESULT 15
US-10-042-431-50
; Sequence 50, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-602
; CURRENT APPLICATION NUMBER: US/10/042.431
; CURRENT FILING DATE: 2001-10-25
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; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-431-50

Query Match 32.8%; Score 700; DB 9; Length 221;
Best Local Similarity 61.0%; Pred. No. 8.1e-62;
Matches 128; Conservative 32; Mismatches 50; Indels 0; Gaps 0;
QY 28 VNPEVMMNTSEIIYNGYSPSEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVYMQHAL 87
DB 8 VDPEAFMNISEIIHQGYPCSEYEVATEDGYILSVNRIPRGLVQPKTGSRPVLLQHGL 67
QY 88 FADNAYWLENYANGSLGFLLDAGYDVWNGSRGNTWSRRHKTLSETDEKFWAFSFDEMA 147
DB 68 VGGASWISNLPNNSLGFILADAGDVWNGSRGNWSRKHKTLSDQDEFWAFSYDEMA 127
QY 148 KYDLPGVIDFIVNKTQGEKLYFIGHSLGTTIGFVAFSTMPPELAQRKMNFMALGPTISFKY 207
DB 128 REDLPAVINFIQKTQGEKLYYVGYSGTGTMGFIASFSTMPPELAQRIKMYFALAPIATVKH 187
QY 208 PTGIFTRFELLPSIHKAVFGTKGFLEDK 237
DB 188 AKSPGTFKLLLPDMMIKGLFGKKEFLYQPR 217

Search completed: April 2, 2003, 16:39:32
Job time : 22 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:23:41 ; Search time 17 seconds
(without alignments)
683.650 Million cell updates/sec

Title: US-10-003-302-2

Perfect score: 2137

Sequence: 1 MMWLLTTTCLICGTNAGG.....FDFVWGLDAPQMFSGNHL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2137	100.0	395	4	US-09-820-001-2
2	1097	51.3	392	4	US-09-820-001-4
3	1017	47.6	380	1	US-08-227-108-16
4	1017	47.6	380	2	US-09-073-674-16
5	1009	47.2	379	1	US-08-227-108-18
6	1009	47.2	379	2	US-09-073-674-18
7	1004	47.0	379	1	US-08-227-108-3
8	1004	47.0	379	2	US-09-073-674-3
9	1004	47.0	380	1	US-08-227-108-5
10	1004	47.0	380	2	US-09-073-674-5
11	1003	46.9	377	1	US-08-227-108-17
12	1003	46.9	377	2	US-09-073-674-17
13	972	45.5	378	4	US-09-186-489-2
14	118.5	5.5	634	1	US-07-779-049-3
15	118.5	5.5	634	1	US-08-080-240-3
16	100	4.7	932	4	US-09-071-035-416
17	100	4.7	969	4	US-09-071-035-414
18	97	4.5	811	1	US-08-136-743B-4
19	96	4.5	262	2	US-08-602-359A-35
20	95	4.4	559	2	US-09-052-339-1
21	95	4.4	559	4	US-09-385-742B-1
22	95	4.4	767	1	US-08-446-777-8
23	93	4.4	444	2	US-08-485-938A-33
24	90.5	4.2	283	4	US-09-134-001C-5652
25	90.5	4.2	318	4	US-09-134-001C-4156
26	90	4.2	286	4	US-09-355-156-9
27	90	4.2	767	1	US-08-446-777-6

28	89.5	4.2	450	1	US-08-188-582-30	Sequence 30, Appl
29	89.5	4.2	450	1	US-08-646-715-30	Sequence 30, Appl
30	89.5	4.2	494	3	US-08-993-260-3	Sequence 3, Appl
31	89	4.2	297	2	US-08-602-359A-37	Sequence 37, Appl
32	88	4.1	574	2	US-08-756-317-4	Sequence 4, Appl
33	88	4.1	600	2	US-08-756-317-3	Sequence 3, Appl
34	88	4.1	638	2	US-08-756-317-2	Sequence 2, Appl
35	86.5	4.0	441	1	US-08-470-187-8	Sequence 8, Appl
36	86.5	4.0	441	1	US-08-318-905-8	Sequence 8, Appl
37	86.5	4.0	441	1	US-08-483-232-8	Sequence 8, Appl
38	86.5	4.0	441	1	US-08-483-140-8	Sequence 8, Appl
39	86.5	4.0	441	2	US-08-485-938A-8	Sequence 8, Appl
40	86.5	4.0	441	2	US-08-910-041-8	Sequence 8, Appl
41	86.5	4.0	441	3	US-09-328-474-8	Sequence 8, Appl
42	86.5	4.0	441	3	US-09-100-546-8	Sequence 8, Appl
43	86.5	4.0	441	4	US-09-010-715-8	Sequence 8, Appl
44	86.5	4.0	441	4	US-09-577-758-8	Sequence 8, Appl
45	86.5	4.0	835	4	US-09-619-333-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-820-001-2
; Sequence 2, Application US/09820001
; Patent No. 6387680
; GENERAL INFORMATION:
; APPLICANT: MERRULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; FILE REFERENCE: CLO01186
; CURRENT APPLICATION NUMBER: US/09/820,001
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Human
US-09-820-001-2

Query Match	100.0%	Score 2137;	DB 4;	Length 395;
Best Local Similarity	100.0%	Pred. No. 3.9e-222;		
Matches	395;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MMWLLTTTCLICGTNAGGFLDLENEVPEVMMTSEIIINYGPSEYEVTTEDGYIL	60	
Db	1	MMWLLTTTCLICGTNAGGFLDLENEVPEVMMTSEIIINYGPSEYEVTTEDGYIL	60	
Qy	61	LVNRIPIYGRTHARSTGPRPVYMOHALFADNAYWLENVANGSLGFLADAGYDVMGNSR	120	
Db	61	LVNRIPIYGRTHARSTGPRPVYMOHALFADNAYWLENVANGSLGFLADAGYDVMGNSR	120	
Qy	121	GNTWSRRKTLTSETDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYFIGHSLGTTIGF	180	
Db	121	GNTWSRRKTLTSETDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYFIGHSLGTTIGF	180	
Qy	181	VAFTSMPELAQRIKMNFFALGPTISFKYPTGIFTRFLPNSIIKAVFGTKGFLEDDKTK	240	
Db	181	VAFTSMPELAQRIKMNFFALGPTISFKYPTGIFTRFLPNSIIKAVFGTKGFLEDDKTK	240	
Qy	241	TASTKICNNKILWLICSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNTHIKOLYH	300	
Db	241	TASTKICNNKILWLICSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNTHIKOLYH	300	
Qy	301	SDEFRAYDGNADNNKHYNQSHPIYDLTAMKVPTAIWAGGHVLTGTPQDVARILPQIK	360	
Db	301	SDEFRAYDGNADNNKHYNQSHPIYDLTAMKVPTAIWAGGHVLTGTPQDVARILPQIK	360	
Qy	361	SLSLVLSLLPEWEPTDFVWGLDAPQMFSGNHL	395	

Db 361 SLVLVLLPEWPTDFVWGLDAPQRMFSGNHL 395

RESULT 2

US-09-820-001-4
; Sequence 4, Application US/09820001
; Patent No. 6387680
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CL001186
; CURRENT APPLICATION NUMBER: US/09/820,001
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Human
US-09-820-001-4

Query Match 51.3%; Score 1097; DB 4; Length 392;
Best Local Similarity 53.6%; Pred. No. 7.1e-110;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;

QY 2 MWLLTTTLCIGTLAGGLDLENVPEVMTSEIIYNGYPSEYEYVTTEDGYILL 61
DB 1 MRELGLVCLVLTWLSHSGGKLTAVDPETNNVSEIISYWGFFSEYLVETEDGYILL 60
QY 62 VNRIPYGRTHARSTGRPPVYVMOHALFADNAYWLENYANGSLGFLADAGYDWMGNSRG 121
DB 61 LNRIPGRKNSDKGPKPVVFLQHLGLDSSNNVTLNANSLGFLADAGYDWMGNSRG 120
QY 122 NWSRRHKLTSETDEKFAFSDDEMAKYDLPVIDFIVNKTGOEKLYFTGHSIGTIGV 181
DB 121 NWSRRHKLTSSQDEFAFSDDEMAKYDLPASINFILNKTGOEQVYVGHSGGTIGFI 180
QY 182 AFTMPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVGTGKGFLEDKTKI 241
DB 181 AFSQIFELAKRKIMFALGPVASFCTSPMAKGLRPLDHLIKDLGKDEFLPQSAFLAW 240
QY 242 ASTKICNNKILMICSEFMSLWAGSNKNNQSMVDMYMSHAPTGSVNHILHIKOLYHS 301
DB 241 LGPHVTHVLKELCGNLCLFLLCGFERNLNMSRDVYTTHTSPAGTSVQNMHLWSQAVF 300
QY 302 DEPRADWGNADNMKHYNSHPPIYDLTAMKVPTAIWAGGHDVLTGTPQDVARILPOIKS 361
DB 301 QKFOAFDMSSAKNYHYNSPTTYNVDMLVPTAVWSGGHDWLDADYDVNILLTQITN 360
QY 362 LSLVLVLLPEWPTDFVWGLDAPQRMFSGNHL 395
DB 361 LVPHES-IPWE-HLDFINGLDAPWRLXNLI 392

RESULT 3

US-08-227-108-16
; Sequence 16, Application US/08227108
; Patent No. 5807726
; GENERAL INFORMATION:
; APPLICANT: Blanchard, Claire
; APPLICANT: Benicourt, Claude
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,108
; FILING DATE: 03-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci, Allan A. 256
; REGISTRATION NUMBER: 7620-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-227-108-16

Query Match 47.6%; Score 1017; DB 1; Length 380;
Best Local Similarity 50.3%; Pred. No. 2.9e-101;
Matches 190; Conservative 68; Mismatches 108; Indels 12; Gaps 4;

QY 14 GTLNAGGLDLENVPEVMTSEIIYNGYPSEYEYVTTEDGYILLVNRIPYGRTHAR 73
DB 3 GKLHFG-----SPEVTMNIOMITYGYPNEEYEVTTEDGYILEVNRIPYKKNKG 53
QY 74 STGPRPVYVMOHALFADNAYWLENYANGSLGFLADAGYDWMGNSRGNTWRRHKLTSE 133
DB 54 NTGQRPVFLQHLGLASATNINLPNNSLAFILADAGYDWMGNSRGNTWRRNLYSP 113
QY 134 TDEKFW-AFSDDEMAKYDLPVIDFIVNKTGOEKLYFTGHSIGTIGFVAFSTMPELAOR 192
DB 114 DSVEFWAFAFSDDEMAKYDLPATIDFIVKTKGQQLHYVGHSGGTIGTAFSTNPSLAKR 173
QY 193 IKMNFALGPTISFKYPTGIFTRFFLLPNSIIKAVGTGKGFLEDKTKIATKICNNKTL 252
DB 174 IRTFVALAPAVATVTKSLINKLRFVPSQLFPIFGDKIFYPHNPFDQFLATEVCSREML 233
QY 253 WLICSEFMSLWAGSNKNNQSMVDMYMSHAPTGSVNHILHIKOLYHSDEFRAVDWGN 312
DB 234 NLLCSNALFICGFSKNTSRLDVLVLSHPAGTSVQNMFWHTQAVKSGKQAYDWGSP 293
QY 313 ADMKHYNSHPPIYDLTAMKVPTAIWAGGHDVLTGTPQDVARILPOIKSLSLVLSLLPEW 372
DB 294 VQNRMYHQSPYVNTAMNVPVIAVWNGKDLLADPQDVGLLLPKLPNL-IYHKBIPIY 352
QY 373 EPTDFVWGLDAPQRMFS 390
DB 353 N-HLDFIWDAPQEVIN 369

RESULT 4

US-09-073-674-16
; Sequence 16, Application US/09073674
; Patent No. 5998189
; GENERAL INFORMATION:
; APPLICANT: Blanchard, Claire
; APPLICANT: Benicourt, Claude
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Road
; CITY: Ann Arbor

STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Crissey, Todd M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072-D1-66-TMC
TELEPHONE: 734 622-7530
TELEFAX: 734 622-1553
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-073-674-16

Query Match 47.6%; Score 1017; DB 2; Length 380;
Best Local Similarity 50.3%; Pred. No. 2.9e-101;
Matches 190; Conservative 68; Mismatches 108; Indels 12; Gaps 4;
Qy 14 GTNAGGFLDLENEVNPVMTSTIIYNGYPSSEYEVTTEDGYILLVNRIPYGRTHAR 73
Db 3 KGLHPG-----SPEVTNISMITYWGPNEEYEVTTEDGYILEVNRIPYGRKNSG 53
Qy 74 STGPRPVVYMHAFADNAYWLENGSLGFLADAGYVWNGSRGTWRRHKTLSL 133
Db 54 NTGQRPVVLQHLGLASATNLSNLPNNLSAFILADAGYVWNGSRGTWARRNLYYSP 113
Qy 134 TDEKFW-AFSEDEMAKYDLPVDFIVNKTQEKLYFGHSLGTTIGFVAESTMPELAQR 192
Db 114 DSVEFWAAFSDEMAKYDLPATIDFIVAKTKGQKOLHYVGHSGQTTIGFIAFSTNPSLAKR 173
Qy 193 IKMNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKTIASTKICNNKIL 252
Db 174 IKTYALAPVATVYTKSLINKLRFVPSQSLFKIFGDKIFYPHNFDDQFLATEVCSREML 233
Qy 253 WLICSEFMSLWAGSNKMMQSDVYVMSHAPTSGSSVHNILHIKOLYHSDEFRAVDWGN 312
Db 234 NLLCSNALFIICGDSKNFNTSRDLVYLSHNPAGTSVQNMFWHTQAVKSGKFAQYDWGSP 293
Qy 313 ADNMKHYNQSHPPYDITAMKVPTAIWAGGHVDVLTGPQDVARIILPOIKSLSLVSLPEW 372
Db 294 VQNRHMYDOSQPPYNTVNTAMVPIAVWNGGKDLLADPDQVGLLPLKPNL-IYHKEIPFY 352
Qy 373 EPTDEVNGLDAPORMFS 390
Db 353 N-HLDFIWMADAPQEVYN 369

RESULT 5
US-08-227-108-18
Sequence 18, Application US/08227108
Patent No. 5807726
GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,108
FILING DATE: 03-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Panucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620-033
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-227-108-18

Query Match 47.2%; Score 1009; DB 1; Length 379;
Best Local Similarity 51.1%; Pred. No. 2.1e-100;
Matches 185; Conservative 69; Mismatches 106; Indels 2; Gaps 1;
Qy 29 NPEVMTSTIIYNGYPSSEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVVYMHQHALF 88
Db 9 NPEVMTSTIIYNGYPSSEYEVTTEDGYILEVNRIPYGRKNSGSRGTWRRHKTLSL 68
Qy 89 ADNAYWLENGSLGFLADAGYVWNGSRGTWRRHKTLSLDEKFWAFSEDEMAK 148
Db 69 ASASNWISNLPNNLSAFILADAGYVWNGSRGTWRRHKTLSLDEKFWAFSEDEMAK 128
Qy 149 YDLPQVDFIVNKTQEKLYFGHSLGTTIGFVAESTMPELAORIKMNFALGPTISFKYPT 208
Db 129 YDLPATIDFIVNKTQEKLYFGHSLGTTIGFVAESTMPELAORIKMNFALGPTISFKYPT 188
Qy 209 TGIFTRFLLPNSIIKAVFGTKGFFLEDKTKTIASTKICNNKILWLCSEFMSLWAGSNK 268
Db 189 KSLVNLKRFIPPTWFKIFGDKIFYPHNFDDQFLATEVCSRETLNVICSNALFIICGDS 248
Qy 269 KMMQSDVYVMSHAPTSGSSVHNILHIKOLYHSDEFRAVDWGNADNMKHYNQSHPPYD 328
Db 249 ANLMSRLDVSVINPAGTSVQNMFWHTQAVKSGKFAQYDWGSP 308
Qy 329 LTAMKVPTAIWAGGHVDVLTGPQDVARIILPOIKSLSLVSLPEWEPTDEVNGLDAPORM 388
Db 309 VTAMVPIAVWNGGKDLLADPDQVGLLPLKPNLIYHKEIP--YNHLDFIWMADAPQEV 366
Qy 389 FS 390
Db 367 YN 368
RESULT 6
US-09-073-674-18
Sequence 18, Application US/09073674
Patent No. 5998189
GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis

; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Road
; CITY: Ann Arbor
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,674
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Crissey, Todd M.
; REGISTRATION NUMBER: 37,807
; REFERENCE/DOCKET NUMBER: 5072-DI-66-TWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 734 622-7530
; TELEFAX: 734 622-1553
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-073-674-18

Query Match 47.2%; Score 1009; DB 2; Length 379;
Best Local Similarity 51.1%; Pred. No. 2.1e-100;
Matches 185; Conservative 69; Mismatches 106; Indels 2; Gaps 1;
QY 29 NPEVMMNTSEIIYNGYSPSEEVTEEDGYILLVNRIPYGRTHARSTGPRPVVYMOHALF 88
DB 9 NPEVNNISOMISYWGYPSEKYEYVTEEDGYILLEVRIPYKKNNGRQRPVVFLOHGLL 68
QY 89 ADNAYWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSSETDEKFWAFSEDEMAK 148
DB 69 ASASNWISNLPNNSLAFILADAGYVWLGNSRGNTWARRNLYYSPDSVEFWAFSEDEMAK 128
QY 149 YDLPGVIDFIVNKTGOEKLYFICHSLGTTIGFVAFSTMPELAQRKIMNPFALGPTTSFKYP 208
DB 129 YDLPATIDFIVKTGOEKLYHVGHSQGTTFIGFIAFSTNPKLAERIKTFYALAPVATVKYT 188
QY 209 TGIFTRFLLPNSIIKAVFGTKGFFLEDDKTKTIASFKICNNKILWILICSEFMSLWAGSNK 268
DB 189 KSLVNLKRIPTMTFKIIFGDKIFPHNFDFDLATQVCSTRTLNVICSNALFIICGFD 248
QY 269 KNNQSRMDVYMSHAPTGSVHNILHILKOLYHSDDEFAYDWMGNADNMKNHYNQSHPPYD 328
DB 249 ANLMSRLDVIYSHNPAGTSVQNMHLWTQAVKSGNFQAEFNWGSQAQNVVHFNQTPPYN 308
QY 329 LTAMKVPTAIWAGGHVLTGTPQDVARILPQIKSLSLVLSLLPEWEPTDFVWGLDAPQRM 388
DB 309 VTAMNVPVIAVWGGNDLADPQDVLDLLPKLSNLIYHKEILP--YNHLDFIWAMNAPQV 366
QY 389 FS 390
DB 367 YN 368

RESULT 7
US-08-227-108-3
; Sequence 3, Application US/08227108
; Patent No. 5807726
; GENERAL INFORMATION:

; APPLICANT: Blanchard, Claire
; APPLICANT: Benicourt, Claude
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,108
; FILING DATE: 03-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci, Allan A.
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 7620-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-227-108-3

Query Match 47.0%; Score 1004; DB 1; Length 379;
Best Local Similarity 50.3%; Pred. No. 7.3e-100;
Matches 182; Conservative 70; Mismatches 108; Indels 2; Gaps 2;
QY 29 NPEVMMNTSEIIYNGYSPSEEVTEEDGYILLVNRIPYGRTHARSTGPRPVVYMOHALF 88
DB 9 NPEVMMNISOMITYWGYPSEEVTEEDGYILLIDRIPYGRKNSENIGRRPVVAFLOHGLL 68
QY 89 ADNAYWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSSETDEKFWAFSEDEMAK 148
DB 69 ASATWISNLPNNSLAFILADAGYDVWLGNSRGNTWARRNLYYSPDSVEFWAFSEDEMAK 128
QY 149 YDLPGVIDFIVNKTGOEKLYFICHSLGTTIGFVAFSTMPELAQRKIMNPFALGPTTSFKYP 208
DB 129 YDLPATIDFIVKTGOEKLYHVGHSQGTTFIGFIAFSTNPKLAERIKTFYALAPVATVKYT 188
QY 209 TGIFTRFLLPNSIIKAVFGTKGFFLEDDKTKTIASFKICNNKILWILICSEFMSLWAGSNK 268
DB 189 ETLNKLMLVSEFLKIFGNKIFYPHHFFDQFLATEVCSTRETVDLLCSNALFIICGDT 248
QY 269 KNNQSRMDVYMSHAPTGSVHNILHILKOLYHSDDEFAYDWMGNADNMKNHYNQSHPPYD 328
DB 249 MNLNMSRLDVIYSHNPAGTSVQNVLHWSQAVKSGFQAFDWSGPVQNMHHTHQSPPYIN 308
QY 329 LTAMKVPTAIWAGGHVLTGTPQDVARILPQIKSLSLVLSLLPEWEPTDFVWGLDAPQRM 388
DB 309 LTDMHVPVIAVWGGNDLADPQDVLDLLPKLSNLIYHKEILP--IYHRKIPPNY--HLDFIWMADAPQAV 366
QY 389 FS 390
DB 367 YN 368

RESULT 8
US-09-073-674-3
; Sequence 3, Application US/09073674


```

: Patent No. 5998189
: GENERAL INFORMATION:
: APPLICANT: Blanchard, Claire
: APPLICANT: Benicourt, Claude
: APPLICANT: Junien, Jean-Louis
: TITLE OF INVENTION: Recombinant Dog Gastric Lipase
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Warner-Lambert Company
: STREET: 2800 Plymouth Road
: CITY: Ann Arbor
: STATE: Michigan
: COUNTRY: U.S.A.
: ZIP: 48105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/073,674
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Crissey, Todd M.
: REGISTRATION NUMBER: 37,807
: REFERENCE/DOCKET NUMBER: 5072-D1-66-TMC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 734 622-7530
: TELEFAX: 734 622-1553
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 379 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-073-674-3

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Query Match 47.0%; Score 1004; DB 2; Length 379;
Best Local Similarity 50.3%; Pred. No. 7.3e-100;
Matches 182; Conservative 70; Mismatches 108; Indels 2; Gaps 2;

Qy 29 NPEVMMNTSEIIYNGYSPSEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVYMQHALF 88
Db 9 NPEVTMNIQSMTYWGYPAAEYEVVTTEDGYILGIDRIPYGRKNSENIGRRPVAFLOHGLL 68
Qy 89 ADNAYWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSSETDEKFWAFSDEMAK 148
Db 69 ASATNWTISNLNPNLSLAFILADAGYDVWLGNSRGNTWARRNLVYSPDSVEFWAFSDEMAK 128
Qy 149 YDLPGVIDFVYKNGTGOEKLXFIHSLGTTIGFVAFSTMPELAQRKMNFGALGPTISFKYP 208
Db 129 YDLPATIDFILKKTGQDKLHVHSGQTTIGFIAFSTNPKLAKRIKTFYALAPVATVKYT 188
Qy 209 TGIETREFLLPNSIIKAVFGTKGFLEDDKTKIASTKCNKILWLICSEFMSLWAGSNK 268
Db 189 ETLLNKLMLVPSFLKFLIFGNKIYPPHFFDQFLATEVCSRETVDLLCSNALFIICGFD 248
Qy 269 KMNQSRMDVYMSHAPTSSVHNILHKLQYHSDERFAYDNGNDADNNKHVNSQSHPPYD 328
Db 249 MNLNMSRLDVLVLSNPACTSVQNLHWSQAVKSGKFOAFDNGSPVQNMHHYHQSMPYYN 308
Qy 329 LTAMKVPTAIWAGGHVILGTPQDVARILPQIKSLVLSLLPEWEPTDFVWGLDAPQRM 388
Db 309 LTDHVPITAVWNGNDLLADPHDVLDDLLSKLPNL-IYHRKIPPNY-HLDFIWMADPOAV 366
Qy 389 FS 390
Db 367 YN 368

RESULT 9

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US-08-227-108-5
: Sequence 5, Application US/082271108
: Patent No. 5807726
: GENERAL INFORMATION:
: APPLICANT: Blanchard, Claire
: APPLICANT: Benicourt, Claude
: APPLICANT: Junien, Jean-Louis
: TITLE OF INVENTION: Recombinant Dog Gastric Lipase
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/227,108
: FILING DATE: 03-APR-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Fanucci, Allan A.
: REGISTRATION NUMBER: 30,256
: REFERENCE/DOCKET NUMBER: 7620-033
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 380 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-227-108-5

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Query Match 47.0%; Score 1004; DB 1; Length 380;
Best Local Similarity 50.3%; Pred. No. 7.4e-100;
Matches 182; Conservative 70; Mismatches 108; Indels 2; Gaps 2;

Qy 29 NPEVMMNTSEIIYNGYSPSEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVYMQHALF 88
Db 10 NPEVTMNIQSMTYWGYPAAEYEVVTTEDGYILGIDRIPYGRKNSENIGRRPVAFLOHGLL 69
Qy 89 ADNAYWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSSETDEKFWAFSDEMAK 148
Db 70 ASATNWTISNLNPNLSLAFILADAGYDVWLGNSRGNTWARRNLVYSPDSVEFWAFSDEMAK 129
Qy 149 YDLPGVIDFVYKNGTGOEKLXFIHSLGTTIGFVAFSTMPELAQRKMNFGALGPTISFKYP 208
Db 130 YDLPATIDFILKKTGQDKLHVHSGQTTIGFIAFSTNPKLAKRIKTFYALAPVATVKYT 189
Qy 209 TGIETREFLLPNSIIKAVFGTKGFLEDDKTKIASTKCNKILWLICSEFMSLWAGSNK 268
Db 190 ETLLNKLMLVPSFLKFLIFGNKIYPPHFFDQFLATEVCSRETVDLLCSNALFIICGFD 249
Qy 269 KMNQSRMDVYMSHAPTSSVHNILHKLQYHSDERFAYDNGNDADNNKHVNSQSHPPYD 328
Db 250 MNLNMSRLDVLVLSNPACTSVQNLHWSQAVKSGKFOAFDNGSPVQNMHHYHQSMPYYN 309
Qy 329 LTAMKVPTAIWAGGHVILGTPQDVARILPQIKSLVLSLLPEWEPTDFVWGLDAPQRM 388
Db 310 LTDHVPITAVWNGNDLLADPHDVLDDLLSKLPNL-IYHRKIPPNY-HLDFIWMADPOAV 367
Qy 389 FS 390
Db 368 YN 369

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RESULT 10

US-09-073-674-5

: Sequence 5, Application US/09073674

: Patent No. 5998189

: GENERAL INFORMATION:

: APPLICANT: Blanchard, Claire

: APPLICANT: Benicourt, Claude

: APPLICANT: Junien, Jean-Louis

: TITLE OF INVENTION: Recombinant Dog Gastric Lipase

: NUMBER OF SEQUENCES: 21

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Warner-Lambert Company

: STREET: 2800 Plymouth Road

: CITY: Ann Arbor

: STATE: Michigan

: COUNTRY: U.S.A.

: ZIP: 48105

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent in Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/073,674

: FILING DATE:

: CLASSIFICATION:

: ATTORNEY/AGENT INFORMATION:

: NAME: Crissey, Todd M.

: REGISTRATION NUMBER: 37,807

: REFERENCE/DOCKET NUMBER: 5072-D1-66-TWC

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 734 622-7530

: TELEFAX: 734 622-1553

: TELEX:

: INFORMATION FOR SEQ ID NO: 5:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 380 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: protein

US-09-073-674-5

Query Match 47.0%; Score 1004; DB 2; Length 380;

Best Local Similarity 50.3%; Pred. No. 7.4e-100;

Matches 182; Conservative 70; Mismatches 108; Indels 2; Gaps 2;

Qy 29 NPEVMMNTSEIIYNGYPSEEEVETEDGYILLVNRIPYGRTHARSTGPRPVYVMOHALF 88

Db 10 NPEVTMISQMTYWGYPFAEEVETEDGYILGIDRIPYGRKNSENIGRRPVAFLOHGLL 69

Qy 89 ADNAYWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSLTDKFWAFSDEMAK 148

Db 70 ASATNWSNLNPNLSLAFILADAGYDVWLGNSRGNTWARRNLYSPDSVEFWAFSDEMAK 129

Qy 149 YDLPGVIDFVNTKGOEKLFTGHSGLTGTIGVAFSTPELAQRKTMFALGPTISFKYP 208

Db 130 YDLPATIDFLKKTQDKLHYVGHSGQTTIGTIAFSTNPKLAKRIKTYALAPVATVKT 189

Qy 209 TGIFTRFLLPNSIIKAVFGTKGFLEDDKTKIASTKICNNKILWLICSEFMSLWAGSNK 268

Db 190 ETLNKLMLVPSFLKFLGKIFYPHFHFDQFLATEVCSRETVDLLCSNALFIICGDET 249

Qy 269 KNNQSRMDVYMSHAPTGSVHNILHIKQLYHSDEFRAVDGNDADNMKHYNQSHPPYD 328

Db 250 MNLNLSRLDVLVSHNPAGTSVQVNLHWSQVSKGFEQAFDWGSPVQNMHHYHQSHPPY 309

Qy 329 LFMKVPITAWAGGHVLTGTPDQVARIILPQIKSLSLVLSLPEWEPPTDFVWGLDAPQRM 388

Db 310 LTFMHPITAVWNGGNDLLADPHDVLKLPNL-IYHRKIPPNY-HLDFIWMADPAQAV 367

Qy 389 FS 390

: :

Db 368 YN 369

RESULT 11

US-08-227-108-17

: Sequence 17, Application US/08227108

: Patent No. 5807726

: GENERAL INFORMATION:

: APPLICANT: Blanchard, Claire

: APPLICANT: Benicourt, Claude

: APPLICANT: Junien, Jean-Louis

: TITLE OF INVENTION: Recombinant Dog Gastric Lipase

: NUMBER OF SEQUENCES: 21

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Pennie & Edmonds

: STREET: 1155 Avenue of the Americas

: CITY: New York

: STATE: New York

: COUNTRY: U.S.A.

: ZIP: 10036

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent in Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/227,108

: FILING DATE: 03-APR-1994

: CLASSIFICATION: 435

: ATTORNEY/AGENT INFORMATION:

: NAME: Panucci, Allan A.

: REGISTRATION NUMBER: 30,256

: REFERENCE/DOCKET NUMBER: 7620-033

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 212 790-9090

: TELEFAX: 212 869-8864/9741

: TELEX: 66141 PENNIE

: INFORMATION FOR SEQ ID NO: 17:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 377 amino acids

: TYPE: amino acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: protein

US-08-227-108-17

Query Match 46.9%; Score 1003; DB 1; Length 377;

Best Local Similarity 50.6%; Pred. No. 9.3e-100;

Matches 183; Conservative 64; Mismatches 113; Indels 2; Gaps 1;

Qy 29 NPEVMMNTSEIIYNGYPSEEEVETEDGYILLVNRIPYGRTHARSTGPRPVYVMOHALF 88

Db 9 NPEAMNISQMTYWGYPQCEVETEDGYILGVYRIPHGKNNSENIGKRPVYLQHGII 68

Qy 89 ADNAYWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSLTDKFWAFSDEMAK 148

Db 69 ASATNWSNLNPNLSLAFILADAGYDVWLGNSRGNTWSRKNVYSPDSVEFWAFSDEMAK 128

Qy 149 YDLPGVIDFVNTKGOEKLFTGHSGLTGTIGVAFSTPELAQRKTMFALGPTISFKYP 208

Db 129 YDLPATINFIQVKTGOEKIHVGHSGQTTIGTIAFSTNPKLAKRIKTYALAPVATVKT 188

Qy 209 TGIFTRFLLPNSIIKAVFGTKGFLEDDKTKIASTKICNNKILWLICSEFMSLWAGSNK 268

Db 189 QSLPKKISFIFTEFLKLMFGKKMFLPHYFDDELGTVECSREVLDLLCSNTLFIICGFDK 248

Qy 269 KNNQSRMDVYMSHAPTGSVHNILHIKQLYHSDEFRAVDGNDADNMKHYNQSHPPYD 328

Db 249 KNLNVSREDVYVGHNPAGTSVQDQLHWAQLVRSKGFEQAFNNGSPSQNMHLHYNQKTPPEYD 308

Qy 329 LFMKVPITAWAGGHVLTGTPDQVARIILPQIKSLSLVLSLPEWEPPTDFVWGLDAPQRM 388

Db 309 VSMTPVAVWNGGNDLLADPHDVLKLPNL-IYHRKIPPNY-HLDFIWMADPAQEV 366

Qy 389 FS 390
Db 367 YN 368

RESULT 12

US-09-073-674-17
; Sequence 17, Application US/09073674
; Patent No. 5998189
; GENERAL INFORMATION:
; APPLICANT: Blanchard, Claire
; APPLICANT: Benicourt, Claude
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Road
; CITY: Ann Arbor
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073.674
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Crissey, Todd M.
; REGISTRATION NUMBER: 37,807
; REFERENCE/DOCKET NUMBER: 5072-D1-66-TMC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 734 622-7530
; TELEFAX: 734 622-1553
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-073-674-17

Query Match 46.9%; Score 1003; DB 2; Length 377;

Best Local Similarity 50.6%; Pred. No. 9.3e-100;

Matches 183; Conservative 64; Mismatches 113; Indels 2; Gaps 1;

Qy 29 NPEVMMNTSEIIINGYPSEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVVYMQHALF 88
Db 9 NPEANMISQMITWGYPCQYEVYTTEDGYILGVYRIPHGKNNSENIGKREPVVYLOHGLI 68
Qy 89 ADNAYWLENYANGSLGFLLDAGYDVWNGSRGNTWSRRHKTSETDEKFWAFSDEMAK 148
Db 69 ASATNWTANLPNNSLAPMLADAGYDVWLGNSRGNTWSRKNNVYSPDSVEFWAFSDEMAK 128
Qy 149 YDLPGVIDFVYNKQGEKLYFIGHSLGTTIGFVAFSTMPELAQRKMNFAFGPTISFKYP 208
Db 129 YDLPATINFVQKTQGEKLYHVGHSQGTIGTGFVAFSTNPTLAKKIKTFYALAPVATVKYT 188
Qy 209 TGIITREFLLPNSIIKAVFGTKGFLEDDKTKIASTKCNKILWLCSEFMSLWAGSNK 268
Db 189 QSLPKKTSFIPTFLFKLMGKMFPHTYFDDELFGVCSREVLDLCSNLFIFCGFDK 248
Qy 269 KNNQSRMDVYMSHAPTSSVHNTHLKHLYHSDERAYDGNADNKKHYNQSHPPYD 328
Db 249 KNLNVSDFVYLGHNPAAGTSVQDFLHWAQLVRSKFGKFAFNWNGSPSNMLHYNQKTPPEYD 308

Qy 329 LTAMKVPTAIWAGGHDVLGTQDVARILPOIKSLVLSLLPEWPTDFVWGLDAPQRM 388
Db 309 VSAMTVPVAVWNGNDILADQDVAMLLPKLSNLLFHKEILA--VNHLDFIWMDAPQEV 366
Qy 389 FS 390
Db 367 YN 368

RESULT 13

US-09-186-489-2
; Sequence 2, Application US/09186489
; Patent No. 6375947
; GENERAL INFORMATION:
; APPLICANT: Bolen, Paul L.
; APPLICANT: Cihak, Paul L.
; APPLICANT: Scharpf Jr., Lewis G.
; TITLE OF INVENTION: Purified Recombinant Kid Pregastric Esterase, and
; FILE OF INVENTION: Processes for its Production and Use
; FILE REFERENCE: 5499/3
; CURRENT APPLICATION NUMBER: US/09/186.489
; CURRENT FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Kid (Goat)
US-09-186-489-2

Query Match 45.5%; Score 972; DB 4; Length 378;

Best Local Similarity 48.6%; Pred. No. 2.1e-96;

Matches 176; Conservative 71; Mismatches 113; Indels 2; Gaps 2;

Qy 29 NPEVMMNTSEIIINGYPSEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVVYMQHALF 88
Db 8 NPEASMNYSQMSIFGWYPSSEMHKVTADGYILQVYRIPHGKNDANHLGQRPVYVFLQHGIL 67
Qy 89 ADNAYWLENYANGSLGFLLDAGYDVWNGSRGNTWSRRHKTSETDEKFWAFSDEMAK 148
Db 68 ASATNWTANLPNNSLGFLLDAGYDVWLGNSRGNTWAEHLVYSPDSVEFWAFSDEMAE 127
Qy 149 YDLPGVIDFVYNKQGEKLYFIGHSLGTTIGFVAFSTMPELAQRKMNFAFGPTISFKYP 208
Db 128 YDLPTIDFILKRTGQKLYHVGHSQGTIGTGFVAFSTNPTLAKKIEVEHALAPVATVKHT 187
Qy 209 TGIITREFLLPNSIIKAVFGTKGFLEDDKTKIASTKCNKILWLCSEFMSLWAGSNK 268
Db 188 QSLFNKALIPHFLFKIIFGNKMFYPHNFPEQFLGVEYCSRETLDVLCKNALFAITGADN 247
Qy 269 KNNQSRMDVYMSHAPTSSVHNTHLKHLYHSDERAYDGNADNKKHYNQSHPPYD 328
Db 248 KNNFMSRLDVYVAINPAGASVQNLHWRQAISKQKQFADWGAASVENLHMHNTPTPIIN 307
Qy 329 LTAMKVPTAIWAGGHDVLGTQDVARILPOIKSLVLSLLPEWPTDFVWGLDAPQRM 388
Db 308 LTAMNVPITAVWSAGODLLADQDVLDDLLLSKLSNL-IHKEIPNPN-HLDFIWMADAPQEV 365
Qy 389 FS 390
Db 366 YN 367

RESULT 14

US-07-779-049-3
; Sequence 3, Application US/0779049
; Patent No. 5310659
; GENERAL INFORMATION:
; APPLICANT: ARAMORI, ICHIRO
; APPLICANT: FUKAGAWA, MASAO
; APPLICANT: ONO, HIROKI
; APPLICANT: ISHITANI, YOSUKE
; APPLICANT: TSUMURA, MANA

APPLICANT: IWAMI, MORITA
APPLICANT: KOJO, HITOSHI
TITLE OF INVENTION: NOVEL GL-7ACA ACYLASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/779,049
FILING DATE: 19911018
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5310659man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-723-0
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 634 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-779-049-3

Query Match 5.5%; Score 118.5; DB 1; Length 634;
Best Local Similarity 20.3%; Pred. No. 0.00064;
Matches 92; Conservative 55; Mismatches 138; Indels 169; Gaps 23;
QY 5 LLTTCCLIGCTLNAGGFLDLENEVPVW---MNTSEII-----IYNGYPSSEY 50
DB 10 MLLTVLVTSLSVAFSGSQEAEELYQYELKTDVMVEMRDGVKLPDIIY--LPVAKT 67
QY 51 EVTTEDGYILLNRIPIYGR--THARSTGPRPVYMQHALFADNAYWLENYANGSLGFLAD 109
DB 68 EQEKKDGFPTLVFRTYPNKDTYKTEGP-----FFAK 99
QY 110 AGYDVMGNSRGNTWSRRHKTLSDEKFWAFSDEMAY--YDL---PGVIDFVKNKTQ 164
DB 100 RGYAVVQDTRG-----RYKSEGE-----WNFVDD-AKGDYDLIEWAAVQDFSTGKVG 148
QY 165 EKLFIHSLGTTIGFVAFSTPELAQRKIMNFALGPTISFKYPTGIFTFRFLPNSIIK 224
DB 149 MGLSYMAY---TQYVLAESKPPHLVTMIPLEGMSNPA-----E 183
QY 225 AVFGTKGFLEDKTKIASTKICNNKILMLICSEFMSLWAG-----SNKKNMQ 273
DB 184 EVFETGGAMQLDR-----YLSWTLGQAVDTFARRLDEKNGNTVQ 222
QY 274 SRM-----DVMMSHAPGSSVHNILHKLQYHSDEFRAWDGNDADNNKHYNQ---SH 323
DB 223 DKIKKALDDYERKWLNHMPRS---KVAPLNQM-----IDWKEAMDPHEDEYWKSI 270
QY 324 PPIYDLTAMKVPATWAGGHDVL--CTPOD-----VARILPOIKSLSLVLS---L 368
DB 271 SQEQHDTPVPVHYHVGWYDILLNGTSKNYIGITENGPTERTYLPALERTVNIQDTQKUL 330
QY 369 LPWE-----PTPDFVWGLDAPQMFSGNHN 394
DB 331 IGPWTHGYQTAVGTFNE-----PKADLSDVHN 358

RESULT 15
US-08-080-240-3
Sequence 3, Application US/08080240
Patent No. 5312750
GENERAL INFORMATION:
APPLICANT: ARAMORI, ICHIRO
APPLICANT: FUKAGAWA, MASAO
APPLICANT: ONO, HIROKI
APPLICANT: ISHITANI, YOSUKE
APPLICANT: TSUMURA, MANA
APPLICANT: IWAMI, MORITA
APPLICANT: KOJO, HITOSHI
TITLE OF INVENTION: NOVEL GL-7ACA ACYLASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/080,240
FILING DATE: 19930622
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5312750man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-803-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 634 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-080-240-3

Query Match 5.5%; Score 118.5; DB 1; Length 634;
Best Local Similarity 20.3%; Pred. No. 0.00064;
Matches 92; Conservative 55; Mismatches 138; Indels 169; Gaps 23;
QY 5 LLTTCCLIGCTLNAGGFLDLENEVPVW---MNTSEII-----IYNGYPSSEY 50
DB 10 MLLTVLVTSLSVAFSGSQEAEELYQYELKTDVMVEMRDGVKLPDIIY--LPVAKT 67
QY 51 EVTTEDGYILLNRIPIYGR--THARSTGPRPVYMQHALFADNAYWLENYANGSLGFLAD 109
DB 68 EQEKKDGFPTLVFRTYPNKDTYKTEGP-----FFAK 99
QY 110 AGYDVMGNSRGNTWSRRHKTLSDEKFWAFSDEMAY--YDL---PGVIDFVKNKTQ 164
DB 100 RGYAVVQDTRG-----RYKSEGE-----WNFVDD-AKGDYDLIEWAAVQDFSTGKVG 148
QY 165 EKLFIHSLGTTIGFVAFSTPELAQRKIMNFALGPTISFKYPTGIFTFRFLPNSIIK 224
DB 149 MGLSYMAY---TQYVLAESKPPHLVTMIPLEGMSNPA-----E 183
QY 225 AVFGTKGFLEDKTKIASTKICNNKILMLICSEFMSLWAG-----SNKKNMQ 273
DB 184 EVFETGGAMQLDR-----YLSWTLGQAVDTFARRLDEKNGNTVQ 222
QY 274 SRM-----DVMMSHAPGSSVHNILHKLQYHSDEFRAWDGNDADNNKHYNQ---SH 323
DB 223 DKIKKALDDYERKWLNHMPRS---KVAPLNQM-----IDWKEAMDPHEDEYWKSI 270

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:39:24 ; Search time 46 Seconds
(without alignments)
825.502 Million cell updates/sec

Title: US-10-003-302-2

Perfect score: 2137

Sequence: 1 MWLLTTTCLICGTLAGG.....FDFVGLDAPQRMFSGNHL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1099	51.4	399	2 G01416	lysosomal acid lip
2	1097	51.3	399	2 S41408	lysosomal acid lip
3	1052	49.2	398	2 S07145	triacylglycerol li
4	1022.5	47.8	395	1 L1RRT	triacylglycerol li
5	982.5	46.0	397	1 JC4017	triacylglycerol li
6	663.5	31.0	405	2 T22675	hypothetical prote
7	644.5	30.2	403	2 T33198	hypothetical prote
8	634	29.7	411	2 T22290	hypothetical prote
9	613	28.7	405	2 H88930	protein R11G11.14
10	585.5	27.4	411	2 G89074	protein K04A8.5 [1
11	546.5	25.6	426	2 T20480	hypothetical prote
12	502.5	23.5	559	2 JT0949	egg-specific prote
13	469.5	22.0	1585	2 T31611	hypothetical prote
14	436	20.4	443	2 T39540	triglyceride lipas
15	405	19.0	467	2 T41053	triglyceride lipas
16	402.5	18.8	344	2 E84526	probable lysosomal
17	347.5	16.3	413	2 T43170	probable triacylg
18	342.5	16.0	548	2 S37969	probable triacylg
19	320	15.0	460	2 T39443	probable triglycer
20	293	13.7	431	2 D86318	protein F15H18.6 [
21	224	10.5	509	2 G96766	protein lipase F2P
22	219.5	10.3	573	2 S64754	probable membrane
23	209	9.8	538	2 S64842	probable membrane
24	147	6.9	336	2 F83425	probable esterase/
25	120	5.6	40	2 S19539	triacylglycerol li
26	118.5	5.5	634	2 I40217	glutaryl 7-ACA acy
27	118	5.5	456	2 E69391	hypothetical prote
28	115	5.4	62	2 S59904	lipase, pregastric
29	111	5.2	297	2 T21632	hypothetical prote

30 111 5.2 300 2 C69664 carboxylesterase N
31 108.5 5.1 300 2 I40425 carboxylesterase (platelet-activatin
32 103.5 4.8 436 2 JC5021 Sd protein - fruit
33 102.5 4.8 363 2 S18765 lipoprotein [impor
34 101.5 4.7 789 2 G50587 laccase (EC 1.10.3
35 101 4.7 573 2 T02743 hypothetical prote
36 100.5 4.7 371 2 T24853 tributyrin esteras
37 100 4.7 259 2 E95071 hypothetical prote
38 100 4.7 259 2 C97939 tributyrin esteras
39 99.5 4.7 185 2 F69767 hypothetical prote
40 99.5 4.7 329 2 D97340 DNA replication pr
41 99.5 4.7 330 2 A10084 thiamin-binding pe
42 99 4.6 804 2 B48687 ribonucleoside-dip
43 98 4.6 286 2 D75217 probable 2-acetyl-
44 98 4.6 1155 2 H71456 probable pyrolysin
45 97.5 4.6 304 2 A89905 hypothetical prote

ALIGNMENTS

RESULT 1

G01416

lysosomal acid lipase - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 18-Jun-1999

C:Accession: G01416

R:Du, H.

submitted to the EMBL Data Library, April 1994

A:Reference number: G06919

A:Accession: G01416

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-399 <DUX>

A:Cross-references: EMBL:U08464; NID:9505052; PIDN:AAB60328.1; PID:9505053

C:Superfamily: triacylglycerol lipase, lingual

C:Keywords: glycoprotein

Query Match 51.4%; Score 1099; DB 2; Length 399;
Best Local Similarity 53.6%; Pred. No. 2.3e-85;
Matches: 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGTLAGGFLDLENEVPEVMMNTSEIIYNGYSPSEYEVETEDGYILL 61
Db 3 MRFLGLVCLVLTLLHSEGRKLTAVDPETNMNVSEIISYWGFPSEYLVETEDGYILC 62
Qy 62 VNRIPYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYVWNGNSRG 121
Db 63 LNRIPHGKRKNSDKGPKPVFLQHGGLADSSNNWVTNLANSLSLGFILADAGFVWNGNSRG 122
Qy 122 NTSRRHKTLSETDEKFWAFSDEMAYDLPQVIDFVNGTGOEKLFIHSLGTTIGFV 181
Db 123 NTSRRHKTLVSQDEFWAFSDEMAYDLPASINFLINKTGOEQVYVGHSGQTIGFI 182
Qy 182 AFSTMPELAQRKMFALGPTISFKYPTGIFTRFELLPNSIIKAVFGTKGFLEDDKTKI 241
Db 183 AFSQIPELAKRIKMFALGPVAVAFCTSPMAKLGRLPDHLKLDLFGDKEFLPQSAFLKW 242
Qy 242 ASTKICNNKIWLICSEFMSLWAGSNKKNQSDMDVMTSHAPTSGSSVHNLIHKQLYHS 301
Db 243 LGTHVCTHVLKELCGNLCLFLLCGFNERNLNMSRDVYVTTTHSPAGTSVQNMLHWSQAVKF 302
Qy 302 DEFAYDWGNDADNKNHYNQSHPIYDLTAMKVPTAIWAGGDDVLGTQDDVARILPOLKS 361
Db 303 QKQAFDMGSSAKNYFHYNQSPPTYNVYKMDLVPYVWSSGGHDLADYVDVNNILLTQITN 362
Qy 362 LSLVLSLLEPEPTDFVWGLDAPQRMFSGNHL 395
Db 363 LVFHES-IPENE-HLDFWGLDAPWRLYNKIINL 394

RESULT 2

S41408

lysosomal acid lipase (EC 3.1.1.-) / sterol esterase (EC 3.1.1.13) precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
 C:Accession: S41408; A39315; S47187
 R:Amels, D.; Merkel, M.; Eckerstorn, C.; Greten, H.
 Eur. J. Biochem. 219, 905-914, 1994
 A:Title: Purification, characterization and molecular cloning of human hepatic lysosomal
 A:Reference number: S41408; MUID:94155897; PMID:8112342
 A:Accession: S41408
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-399 <AME>
 A:Cross-references: EMBL:X76488; NID:g434305; PIDN:CAA54026.1; PID:g434306
 R:Anderson, R.A.; Sando, G.N.
 J. Biol. Chem. 266, 22479-22484, 1991
 A:Title: Cloning and expression of cDNA encoding human lysosomal acid lipase/cholesteryl
 A:Reference number: A39315; MUID:92042192; PMID:1718995
 A:Accession: A39315
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-15, 'P', 17-399 <AND>
 A:Cross-references: GB:M74775; NID:g187151; PIDN:AAA59519.1; PID:g187152
 R:Du, H.; Gregory, G.A.
 Submitted to the EMBL Data Library, April 1994
 A:Description: Structural conservation of putative functional motifs between mouse and h
 A:Reference number: S47187
 A:Accession: S47187
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-22, 'R', 24-399 <DUH>
 A:Cross-references: EMBL:D31690; NID:g506430; PIDN:CAA83495.1; PID:g506431
 C:Genetics:
 A:Gene: GDB:LIPA
 A:Cross-references: GDB:120153; OMIM:278000
 A:Map position: 10q24-10q25
 C:Superfamily: triacylglycerol lipase, lingual
 C:Keywords: carboxylic ester hydrolase; glycoprotein

Query Match 51.3%; Score 1097; DB 2; Length 399;
 Best Local Similarity 53.6%; Pred. No. 3.4e-85;
 Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;

QY 2 MWLLTTTCLICGTLNAGGFLENEVNPVMWNTSEIIYNGYPSSEYEVTTEDGYILL 61
 DB 3 MRFGLVCLVLTWTHSESGGKLTAVDPETNMNVSEIISYWGFFSEYLVETEDGYILL 62
 QY 62 VNRIPYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
 DB 63 LNRIPGRKHNHSDGPKPVVFLQHLGLADSSNWNVLNSSLGFLADAGYDVWNGNSRG 122
 QY 122 NTWSRRHKTLSSETDEKFAFSDDEMAKYDLPVIDFVKNKTGOEKLIFYGHSLGTTIGFV 181
 DB 123 NTWSRRHKTLSVSQDEFWAFSDDEMAKYDLPASINFILNKTGOEQVYVGHSGQTTIGFI 182
 QY 182 AFTMPQLAQRKIMFALGPTISFKYPTGIFTRFFLLPNSIIKAVGTFKGFLEDDKTKI 241
 DB 183 AFSQIPQLAKRIMFALGPTISFKYPTGIFTRFFLLPNSIIKAVGTFKGFLEDDKTKI 242
 QY 242 ASTKCNKILMLICSEFMSLWAGSNKNNOSRMDVYMSHAPTSSSVNHLHIKQLYHS 301
 DB 243 LGTHVCTHVLKELGNCILFLLCGNERNLNSRDVYTHSPAGTSVQNMHLHWSQAVKF 302
 QY 302 DEFRAVDGNDADNNKHYNQSHPPYDILTMKVPTAINAGGHDVLGTPODVARILPOIKS 361
 DB 303 QKQAFDWSGSSAKNFHYNQSPYPTYNVKNMVLVPTAVNSGGHDLADVVYDVNILLTQTIN 362
 QY 362 LSLVLSLLPEWPTDFVWGLDAPQRMFSGNHL 395
 DB 363 LVFHES-IPWE-HLDFIWGLDAPRLYNKIINL 394

RESULT 3
 S07145

triacylglycerol lipase (EC 3.1.1.13) precursor, gastric - human
 C:Species: Homo sapiens (man)
 C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 18-Jun-1999
 C:Accession: S07145; S27102; S04942
 R:Boomer, M.W.; Angal, S.; Farranton, G.T.; Harris, T.J.R.; Lyons, A.; King, D.J.; Pi
 Biochim. Biophys. Acta 909, 237-244, 1987
 A:Title: Molecular cloning of a human gastric lipase and expression of the enzyme in
 A:Reference number: S07145; MUID:87299724; PMID:3304425
 A:Accession: S07145
 A:Molecule type: mRNA
 A:Residues: 1-398 <BODI>
 A:Cross-references: EMBL:X05997; NID:g31771; PIDN:CAA29413.1; PID:g758063
 A:Accession: S27102
 A:Molecule type: protein
 A:Residues: 20-24, 'X', 26, 'X', 28-33, 'X', 35-42, 'X', 44, 'X', 46-48, 'X', 50, 'X', 52, 'X', 54-56
 A:NOTE: it is uncertain whether Met-1 or Met-7 is the Initiator
 R:Bernbeck, S.; Blaackberg, L.
 Eur. J. Biochem. 182, 495-499, 1989
 A:Title: Human gastric lipase. The N-terminal tetrapeptide is essential for lipid bin
 A:Reference number: S04942; MUID:89325292; PMID:2753032
 A:Accession: S04942
 A:Molecule type: protein
 A:Residues: 20-45 <BER>
 C:Superfamily: triacylglycerol lipase, lingual
 C:Keywords: carboxylic ester hydrolase; extracellular protein; glycoprotein; lipid di
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-398/Product: triacylglycerol lipase, gastric #status experimental <MAT>
 F:34,99,185,271/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.2%; Score 1052; DB 2; Length 398;
 Best Local Similarity 50.4%; Pred. No. 2.2e-81;
 Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;

QY 2 MWLLTTTCLICGTLNAGGFLENEVNPVMWNTSEIIYNGYPSSEYEVTTEDGYILL 61
 DB 1 MWLLTMTASLISVLGTHGLFKLHPGSEPTVMTNISQMTYWGYNVEEYEVTTEDGYILL 60
 QY 62 VNRIPYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
 DB 61 VNRIPYGRKNSGNTGPRPVVFLQHLGLASATNWNISLNPNSLAFILADAGYDVWNGNSRG 120
 QY 122 NTWSRRHKTLSSETDEKFAFSDDEMAKYDLPVIDFVKNKTGOEKLIFYGHSLGTTIGFV 181
 DB 121 NTWARMNLYSPDSVEFWAFSDDEMAKYDLPATIDFVAKTKQKQLHYVGHSGQTTIGFI 180
 QY 182 AFTMPQLAQRKIMFALGPTISFKYPTGIFTRFFLLPNSIIKAVGTFKGFLEDDKTKI 241
 DB 181 AFTNPSLAKRIKTYALAPVATVYTKSLINKLRFVPSQSLFKFIFGDKIFYPHNFDDQF 240
 QY 242 ASTKCNKILMLICSEFMSLWAGSNKNNOSRMDVYMSHAPTSSSVNHLHIKQLYHS 301
 DB 241 LATEVCSREMLNLCSNALFIICGFSKFNFTSRDLVYLSHNPAGTSVQNMHFWHTQAVKS 300
 QY 302 DEFRAVDGNDADNNKHYNQSHPPYDILTMKVPTAINAGGHDVLGTPODVARILPOIKS 361
 DB 301 GRQAYDNGSPVONRMHVDQSQPPYINVTAMNVPYAVWNGGKDLLADPDQVGLLLPKLPN 360
 QY 362 LSLVLSLLPEWPTDFVWGLDAPQRMFS 390
 DB 361 L-IYHKEIPFYN-HLDFIWAMDAPQEVYN 387

RESULT 4
 LIPT
 triacylglycerol lipase (EC 3.1.1.13) precursor, lingual - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 11-Jun-1999
 C:Accession: A23045
 R:Doeherty, A.J.P.; Bodmer, M.W.; Angal, S.; Verger, R.; Riviere, C.; Lowe, P.A.; Lyo
 Nucleic Acids Res. 13, 1891-1903, 1985
 A:Title: Molecular cloning and nucleotide sequence of rat lingual lipase cDNA.
 A:Reference number: A23045; MUID:85215587; PMID:3839077
 A:Accession: A23045

RESULT 6
T22675
hypothetical protein F54F3.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 21-Jan-2000

```

RESULT 6
T22675 hypothetical protein F54F3.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T22675
R:Percy, C.; Lloyd, C.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z19598
A:Accession: T22675
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-405 <WIL>
A:Cross-references: EMBL:Z79696; PIDN:CAB01973.1; GSPDB:GN00023; CESP:F54F3.3
A:Experimental source: clone F54F3
C:Genetics:
A:Gene: CESP:F54F3.3
A:Map position: 5
C:Superfamily: triacylglycerol lipase, lingual

Query Match          31.0%;   Score 663.5;   DB 2;   Length 405;
Best Local Similarity 37.8%;   Pred. No. 2.le-48;
Matches 151; Conservative 68; Mismatches 154; Indels 27; Gaps

QY    1 MWVLLLTTCCTLCCTAGGFLDENLVNPVEVMWNTSEIIINYGYPSEEVEVTEDGYIL 60
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db     7 VMLAVLAATAATVFG-----HDADPEMKMTTFQIIMRWGYFAMIYDVTTEGYIL 55

QY    61 LVNRPYGRTHAR-STGPRPVVMYMQHAFENADNYAWLENANGSLGLLADAGYDVWMGNS 119
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db     56 ELHRIPYGKTNVWPNGCKPVVFQMQLCESSNWVNLPTESNAFLFDAGGYDVLGNF 115

QY    120 RGNTWSRRHKTLGETDEKFVAFSDEMAYKYLDLPGVIDFIYNVKTKYFIGHSLSGTTTG 179
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

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Db 116 RGNTYSMKHNKLNKPSHSFAFDWGSWDEMQQVDLPAMTEKALEVTGQDSLYYIGHSGGT--- 172
QY 180 FVAFSTMP-----LAORIKMNFALGPTISFKYPTG---IFTRFFLLPNSEIIKAVFTKGF 232
Db 173 LTFESRLSEDKVGWGNKIKFFALAPVGSVKHILGALKFFADYFSLFFDGFDFVSGSEF 232
QY 233 FLEDKTKTIASTKICNN-KILMKILSEFMSLNAGSNKKNMNSRMDVYMSHAPTGSVVHN 291
Db 233 LPNNWIMKLVSSEVCAGLKEACGVCDVWFLLIAGPESQNLNATRPVIYVAHTPAGTSTQN 292
QY 292 ILHIKQLYHSEFRAYDWGNDAENMKHYNQSHPPYIDLTKMKVPTAINAGGHDVILGTQD 351
Db 293 IVHIQAVRRHGGETPKYDYG-EKNGKHHYQGANYPAYDFTVTRPVLYWGDSDWLADPTD 351
QY 352 VARTLPQIKSLSLVL--SLLPEWEPTFDFVWGLDAPQRMF 389
Db 352 VTDFLLTHLNPSTVQNNKLIDYN-HLDFIWLGRAPKDIY 390

RESULT 7
T33198
hypoetical protein ZK6.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C:Accession: T33198
R:WU, X
Submitted to the EMBL Data Library, May 1998
A:Description: The sequence of C. elegans cosmid ZK6.
A:Reference number: Z21301
A:Accession: T33198
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-403 <WUX>
A:Cross-references: EMBL:AF067942; PIDN:AAC17694.1; GSPDB:GN00023; CESP:ZK6
A:Experimental source: strain Bristol N2; clone ZK6
C:Genetics:
A:Gene: CESP:ZK6.7
A:Map position: 5
A:Introns: 29/3; 63/1; 219/3; 319/3; 365/3
C:Superfamily: triacylglycerol lipase, linqual

```

RESULT 8

[illegible]

RESULT 12

JT0949
egg-specific protein - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 26-Feb-1998
C:Accession: JT0949; A28527
R:Sato, Y.; Yamashita, O.
submitted to JIPID, September 1991
A:Reference number: JT0949
A:Accession: JT0949
A:Molecule type: DNA
A:Residues: 1-559 <SAT>
A:Experimental source: larva
A:Note: this protein is a homotrimer
R:Indraaith, L.S.; Sasaki, T.; Yamashita, O.
J. Biol. Chem. 263, 1045-1051, 1988
A:Title: A unique protease responsible for selective degradation of a yolk protein in Bombyx mori
A:Reference number: A28527; MUID:88087166; PMID:3275655
A:Accession: A28527
A:Molecule type: protein
A:Residues: 19-40:133-144, 'T', 146-152:229-248 <IND>
C:Genetics:
A:Map position: 19
C:Keywords: egg yolk; homotrimer
F:132-133/Cleavage site: Lys-Asn (egg 30.5K cysteine proteinase) #status experimental
F:228-229/Cleavage site: Arg-Asp (egg 30.5K cysteine proteinase) #status experimental

Query Match 23.5%; Score 502.5; DB 2; Length 559;
Best Local Similarity 32.7%; Pred. No. 1.5e-34;
Matches 128; Conservative 63; Mismatches 154; Indels 47; Gaps 13;
QY 23 DLENEVNEVWNTSEIIINYGYPSSEYEVTTEDGYLLVNRIPYGRTH-ARSTGPRPV 81
DB 179 ETQRENEDFHLNATELLKHKQYPVEETHVATDDGYHLTVLRIP--PTHQTRDDKKKPPVA 236
QY 82 YMOHALFADNAVLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSLTDKFKWAF 141
DB 237 LMGHLLGSADWLLMGFSKSLAYLSDAGYDVWLVNVRGNKYSRSHVSKHPALNDFKWF 296
QY 142 SPDEMAKYDLPQGVDFIVNKTQGEKLYFIGHSLGTIGTFVAFSTMPPELAQRKMMNFGALGP 201
DB 297 SNDEIALHDLPAILDVLHSDISQERLHYGHSGQATTFEALMSQEPSYNEKIVSMHALSP 356
QY 202 TISFYK-----PTGIFTRF-----LLPNSLIKAVFGTKFFLEDKKTKTAS 243
DB 357 IYMNIVRSPLFRMTAPTSKEYQYIHDQVGHGAFEPGKHLIETFGGAAC-----REKLGC 411
QY 244 TKICNKKILWLICSEFMSIWSGSKNNQSRMDVYMSHAPTGSVVHNLILKOLYHSD 303
DB 412 RHVCNN-LNYVI-----SGINYNQDADIVPVVMAHLPAAGTSARVKNQYQGNVASHD 462
QY 304 FRAYDWGNDADNKNHNSHPPIYDLTAMKVPTAIWAGGHV-LGTPOQDVARI---LPQI 359
DB 463 FRKYNAGET-NMKYVGASEPYSYDLKSVSPVNLV-HSHDAWLAHPKDVKEKLENLPV 520
QY 360 KSLSLVLSLLPWE---PTDFVWGLDAPQRMF 389
DB 521 KQSFEV----PQQHFTDLDFQFSKAPDVTY 548

RESULT 13

T31611
hypotheoretical protein Y5088A.g - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31611
R:Steward, C.
submitted to the EMBL Data Library, September 1999
A:Reference number: #21047
A:Accession: T31611
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-1585 <WIL>

A:Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CAB55050.1; CESP:Y5088A.g
A:Experimental source: clone Y5088A

C:Genetics:

A:Gene: CESP:Y5088A.g
A:Introns: 25/3; 60/1; 133/2; 217/3; 270/3; 337/2; 400/1; 746/2

Query Match 22.0%; Score 469.5; DB 2; Length 1585;
Best Local Similarity 31.6%; Pred. No. 4.1e-31;
Matches 117; Conservative 67; Mismatches 171; Indels 15; Gaps 7;

QY 31 EWMNTSEIIINYGYPSSEYEVTTEDGYLLVNRIPYGRTHARSTG--PRPVVYMQHALF 88
DB 20 EETLDAADTISHYGYTVEKHVYTTDDGYTVQLQRIPIVGRDDRSILGCSKRPVVFEMHGLF 79
QY 89 ADNAVWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSLTDKFKWAFSDEMAK 148
DB 80 GSSYHFLNLPQSAAYIFADAGFDVWGLNRTGYELNHTFSFNGVFNWFSLEYHSH 139
QY 149 YDLPGVDFIVNKTQGEKLYFIGHSLGTIGTFVAFSTMPPELAQ-RIKMNFALGPTISFKY 207
DB 140 YDLROOIEYVLDYTRHESLFYVGHSGQTAVMPARLAEADVTWQSKIRVFFALGPTAGFMK 199
QY 208 PTGIFTRFELLPNSIIKAVF-----GTRGFFLEDRKTKIAS--TKICNKKILWLICSEFM 260
DB 200 PLMPT-----LLEENYLOALIQFALDQKFGILLPVEIPRAIASKAFADFCSSKPFTELCSAGF 256
QY 261 SLWAG-SNKKMNSQSRMDVYMSHAPTGSVVHNLILKOLYHSDPRAYDWGNDADNKNHY 319
DB 257 KVAAGIETLGOVNDSRIPILSHFPSATSTLLHWMQIFKYHELRRLDLGT-ARNLIAY 315
QY 320 NQSHPIYDLTAMKVPTAIWAGGHVLTGPQDVARILPOIKSLSLVLSLLPWEPTDFV 379
DB 316 GOKDAPRLEIGNIIAQTILYFSKDDQITDEVVDRELIIMKQMGPGGLIESYDLDFHFTDFEI 375
QY 380 WGLDAPQRMF 389
DB 376 LGLRATDEVY 385

RESULT 14

T39540
triglyceride lipase-cholesterol esterase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: T39540
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
submitted to the EMBL Data Library, February 1998
A:Reference number: 221862
A:Accession: T39540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-443 <WOO>
A:Cross-references: EMBL:AL021748; PIDN:CAA16863.1; GSPDB:GN00067; SPDB:SPBC16A3.12c
A:Experimental source: strain 972h-; cosmid c16A3
C:Genetics:
A:Gene: SPDB:SPBC16A3.12c
A:Map position: 2
A:Introns: 11/2; 152/3; 282/1; 398/3
C:Superfamily: triacylglycerol lipase, lingual

Query Match 20.4%; Score 436; DB 2; Length 443;

Best Local Similarity 31.7%; Pred. No. 4.7e-29;
Matches 116; Conservative 68; Mismatches 150; Indels 32; Gaps 12;
QY 35 NTSEIIINYGYPSSEYEVTTEDGYLLVNRIPYGRTHAR-STGPRPVVYMQHALFADNAY 93
DB 74 NIYEICEAFGYVEEHLVYRTQDNFILCLHRI---THPKSQSHKREVYVCHHGLMTNSEL 129
QY 94 MLE-NYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSLTDKFKWAFSDEMAKYDLP 152
DB 130 WVAVNESRSLPFFVLIESGYDWLGNRGNKYSRKHITYKPKDEBFNFWFLSDMAFMFDIP 189

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:35:32 ; Search time 19 seconds
(without alignments)
862.271 Million cell updates/sec

Title: US-10-003-302-2

Perfect score: 2137

Sequence: 1 MMWLLTTTCLICGTLNAGG.....FDFVWGLDAPQRMFSGNHNL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	1091	51.1	399	1 LICH_HUMAN	P38571 homo sapien
2	1052	49.2	398	1 LIPG_HUMAN	P07098 homo sapien
3	1031	48.2	398	1 LIPG_CANFA	P80035 canis famli
4	1022.5	47.8	395	1 LIPG_RAT	P04634 rattus norv
5	1015	47.5	397	1 LICH_RAT	Q64194 rattus norv
6	982.5	46.0	397	1 LIPG_BOVIN	Q29458 bos taurus
7	980.5	45.9	397	1 LICH_MOUSE	Q920m5 mus musculu
8	533	24.9	394	1 LIP3_DROME	O46108 drosophila
9	486	22.7	439	1 LIP1_DROME	O46107 drosophila
10	342.5	16.0	548	1 TGL1_YEAST	P34163 saccharomyc
11	103.5	4.8	436	1 PAFA_CAVPO	P70683 c platelet-
12	102	4.8	349	1 HS2S_DROME	P25722 drosophila
13	99.5	4.7	185	1 YCZH_BACSU	O31482 bacillus su
14	99	4.6	804	1 RIR1_PLAFG	P50647 plasmodium
15	97	4.5	277	1 BPHD_PSES1	P17548 pseudomonas
16	96.5	4.5	879	1 YE07_MYCPN	P75377 mycoplasma
17	94	4.4	445	1 SPRI_YEAST	P32603 saccharomyc
18	93	4.4	444	1 PAFA_BOVIN	Q28017 b platelet-
19	92.5	4.3	268	1 ESL2_MYCPN	P75311 mycoplasma
20	91	4.3	1864	1 VGNB_RCMV	P35930 red clover
21	90.5	4.2	1680	1 CO5_MOUSE	P06684 mus musculu
22	90	4.2	404	1 Y432_MYCPN	P75166 mycoplasma
23	89.5	4.2	428	1 YE63_SCHPO	O14249 schizosacch
24	89.5	4.2	910	1 SC15_YEAST	P22224 saccharomyc
25	89	4.2	857	1 LOX3_SOYBN	P09186 glycine max
26	88.5	4.1	423	1 P47A_CANBO	P21245 candida boi
27	88.5	4.1	1046	1 K052_HUMAN	P42285 homo sapien
28	87	4.1	860	1 KDPO_MYCTU	P96372 mycobacteri
29	87	4.1	1155	1 RPOB_BORBU	O59191 borrelia bu
30	87	4.1	3744	1 YHP9_YEAST	P38811 saccharomyc
31	86.5	4.0	441	1 PAFA_HUMAN	Q13093 h platelet-
32	86.5	4.0	1409	1 HAP1_HAFIN	P44596 haemophilus
33	86	4.0	643	1 GYRB_MYCCA	P50028 mycoplasma

RESULT 1

ID	LICH_HUMAN	STANDARD:	PRT:	399 AA.
AC	P38571: 016529; Q96EJO:			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lysosomal acid lipase/cholesterol ester hydrolase precursor			
DE	(EC 3.1.1.13) (LAL) (Acid cholesterol ester hydrolase) (Sterol			
DE	esterase) (Lipase A) (Cholesteryl esterase).			
GN	LIPA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 196-212; 277-297 AND 305-315.			
RX	MEDLINE=92042192; PubMed=1718995;			
RA	Anderson R.A., Sando G.N.;			
RT	"Cloning and expression of cDNA encoding human lysosomal acid			
RT	lipase/cholesterol ester hydrolase. Similarities to gastric and			
RT	lingual lipases.";			
RL	J. Biol. Chem. 266:22479-22484(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=94155897; PubMed=8112342;			
RA	Ameis D., Merkel M., Eckerskorn C., Greten H.;			
RT	"Purification, characterization and molecular cloning of human			
RT	hepatic lysosomal acid lipase.";			
RL	Eur. J. Biochem. 219:905-914(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=96363957; PubMed=8725147;			
RA	Du H., Witte D.P., Grabowski G.A.;			
RT	"Tissue and cellular specific expression of murine lysosomal acid			
RT	lipase mRNA and protein.";			
RL	J. Lipid Res. 37:937-949(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	Strausberg R.;			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	VARIANT CSD/WD PRO-200.			
RX	MEDLINE=94195814; PubMed=8146180;			
RA	Anderson R.A., Byrum R.S., Coates P.M., Sando G.N.;			
RT	"Mutations at the lysosomal acid cholesterol ester hydrolase gene			
RT	locus in Wolman disease.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2718-2722(1994).			
RN	[6]			
RP	VARIANTS CSD ARG-129 AND PRO-129.			
RX	MEDLINE=98295576; PubMed=9633819;			
RA	Ries S., Buechler C., Schindler G., Aslanidis C., Gasche C.,			
RA	Jung N., Schambach A., Fehrer P., Vanier M.T., Belli D.C.,			

ALIGNMENTS

P03593 alfalfa mos
Q53654 staphylococ
Q07121 arthrobacte
Q07123 arthrobacte
P39985 saccharomyc
P19097 s fatty aci
Q9qzy8 cavia porce
P29016 homo sapien
O46051 drosophila
P81171 rickettsia
P32480 saccharomyc
P55895 homo sapien

V90K_AMVLE
CNA_STAAU
AMOL_ARTS1
AMOL_ARTS1
DPOS_YEAST
FAS2_YEAST
CIC1_CAVPO
CD1B_HUMAN
C4DE_DROME
Y174_RICPR
HIR2_YEAST
RAG2_HUMAN

86
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85.5
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85
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84.5
84.5
84.5
84.5
84.5
84

1
1
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1

RA Greten H., Schmitz G.;
RT "Different missense mutations in histidine-108 of lysosomal acid
RT lipase cause cholesteryl ester storage disease in unrelated compound
RT heterozygous and hemizygous individuals.";
RL Hum. Mutat. 12:44-51(1998).
CC -!- FUNCTION: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL
CC ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTOR-
CC MEDIATED ENDOCYTOSIS OF LIPOPROTEIN PARTICLES. IMPORTANT IN
CC MEDIATING THE EFFECT OF LDL (LOW DENSITY LIPOPROTEIN) UPTAKE ON
CC SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION
CC OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION.
CC -!- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC acid.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- DISEASE: DEFECTS IN LIPA ARE THE CAUSE OF THE SEVERE INFANTILE-
CC ONSET WOLMAN DISEASE (WD) AND THE MILDER LATE-ONSET CHOLESTERYL
CC ESTER STORAGE DISEASE (CESD).
CC -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC -----
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CC -----
DR EMBL; M74775; AAB59519.1; -;
DR EMBL; U04285; AAB60327.1; -;
DR EMBL; U04286; AAB60327.1; JOINED.
DR EMBL; U04287; AAB60327.1; JOINED.
DR EMBL; U04288; AAB60327.1; JOINED.
DR EMBL; U04290; AAB60327.1; JOINED.
DR EMBL; U04291; AAB60327.1; JOINED.
DR EMBL; U04292; AAB60327.1; JOINED.
DR EMBL; U04293; AAB60327.1; JOINED.
DR EMBL; U04294; AAB60327.1; JOINED.
DR EMBL; X76488; CAA54026.1; -;
DR EMBL; M731690; CAA83495.1; -;
DR EMBL; U08464; AAB60328.1; -;
DR EMBL; BC012287; AAB12287.1; -;
DR PIR; A39315; A39315.
DR Genew; HGNC:6617; LIPA.
DR MIM; 278000; -;
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser esters_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal; Lysosome;
KW Disease mutation; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 399
FT
FT ACT_SITE 174
FT ACT_SITE 374
FT CARBOHYD 36
FT CARBOHYD 72
FT CARBOHYD 101
FT CARBOHYD 161
FT CARBOHYD 273
FT CARBOHYD 321
FT VARIANT 16
FT
FT VARIANT 129
FT
FT VARIANT 129
FT
FT VARIANT 200
FT
FT CONFLICT 23
FT CONFLICT 29
FT SEQUENCE 399 AA; 45415 MW; 55F27391306B609A CRC64;

Query Match 51.1%; Score 1091; DB 1; Length 399;
Best Local Similarity 53.3%; Pred. No. 3.7e-82;
Matches 210; Conservative 63; Mismatches 119; Indels 2; Gaps 2;
QY 2 MWLLTTTCLICGTNAGGFLDLENEVPVWMTSEIIIIYNGYSEYEVETEDGYILL 61
DB 3 MRLGLVCLVLPVHSEGGKLTAVDPETNMNYSIIISYWGFPSEYLVETEDGYILL 62
QY 62 VNIPIYGTTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
DB 63 LNIPIHGRNHNKDKPKPVFLQRLGLADSSNWNINLANSSLGFLADAGYDVMGNSRG 122
QY 122 NTSRRHKTLSDEKFWAFSEDEMAKYDLPGVIDFIYVNTKQOEKLYFTGHSLGTIGV 181
DB 123 NTSRRHKTLSVSDQEFWAFSEDEMAKYDLPASINFILNKTGOEQVYVGHSGQTIGI 182
QY 182 ARSTPELAORIKMNFALGPTISFKYPTGIFTRFELLPSIIKAVGKGFPLEDKTKFI 241
DB 183 AFSQIPELAKRIKMFALGPVAVAFCTSPMAKLGRLPDHLIKDLFGDKEFLPQSAFLKW 242
QY 242 ASTKICNNKILWLCSEFMSLWAGSNKNMOSRMDVYMSHAPTSSVHNILRIQLYHS 301
DB 243 LGTHVCTHVLKELCGNLCFLCGENRNLNMSRDVYTHSPAGTSVQNMHLHWSQAVKF 302
QY 302 DEFRAIDMGNDADNKHYNQSHPPYIDLTAMKVPTAINAGGHDVILGTPODVARILPQIKS 361
DB 303 QKQFAFDGSSAKNYFHYNQSPYPTYNVKDMLVPTAVMSGGHDLADVYDVNILLTQITN 362
QY 362 LSLVLSLPEWEPTDFVWGLDAPQPMFSGNHL 395
DB 363 LVFHES-IPWE-HLDFWGLDAPWRLYNKIINL 394
RESULT 2
LIPG_HUMAN
ID LIPG_HUMAN STANDARD; PRT; 398 AA.
AC P07098;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) (Gastric
DE lipase) (GL).
GN LIPF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299724; PubMed=3304425;
RA Bodmer M.W., Angal S., Yarranton G.T., Harris T.J.R., Lyons A.,
RA King D.J., Pieroni G., Riviere C., Verger R., Lowe P.A.;
RT "Molecular cloning of a human gastric lipase and expression of the
RT enzyme in yeast.";
RL Biochim. Biophys. Acta 909:237-244(1987).
RN [2]
RP SEQUENCE OF 20-45.
RX MEDLINE=89325292; PubMed=2753032;
RA Bernbaeck S., Blaackberg L.;
RT "Human gastric lipase. The N-terminal tetrapeptide is essential for
RT lipid binding and lipase activity.";
RL Eur. J. Biochem. 182:495-499(1989).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RP MEDLINE=99287897; PubMed=10358049;
RA Roussel A., Canaan S., Egloff M.P., Riviere M., Dupuis L., Verger R.,
RA Cambillau C.;
RT "Crystal structure of human gastric lipase and model of lysosomal
RT acid lipase, two lipolytic enzymes of medical interest.";
RL J. Biol. Chem. 274:16995-17002(1999).
CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -!- SUBCELLULAR LOCATION: Secreted.


```

CC CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC CC -----
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CC CC -----
DR EMBL; X05997; CAA29413.1; -;
DR EMBL; X05997; CAA29414.1; ALT_INIT.
DR EMBL; A01046; CAA00125.1; -;
DR EMBL; A12714; CAA01053.1; -;
DR PIR; S04942; S04942.
DR PIR; S07145; S07145.
DR PDB; 1HLG; 15-MAR-00.
DR Genew; HGNC:6622; LIPF.
DR MIM; 601980; -;
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal; Polymorphism;
FT 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 398 TRIACYLGLYCEROL LIPASE, GASTRIC.
FT ACT_SITE 172 172 CHARGE RELAY SYSTEM.
FT ACT_SITE 343 343 CHARGE RELAY SYSTEM.
FT ACT_SITE 372 372 CHARGE RELAY SYSTEM.
FT DISULFID 246 255
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .).
FT CARBOHYD 327 327 T -> A (IN DBSNP:814628).
FT VARIANT 161 161 /FTID=VAR_011947.
SQ SEQUENCE 398 AA; 45237 MW; CD3EE1621C014F0F CRC64;

Query Match 49.2%; Score 1052; DB 1; Length 398;
Best Local Similarity 50.4%; Pred. No. 5.8e-79;
Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGLTLAGGFLDLENEVNPVMMTSEIIINGYPSEYEVTTEDGYILL 61
Db 1 MWLLTASLSVLGTTGLGFKLHGPSPEVTMISQMTITWGPNEEYEVTTEDGYILE 60

Qy 62 VNRIPIGTRHARSTGRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
Db 61 VNRIPIGKNSGNTQRPVFLQGLLASATNWSLNPLNNSLAFLADAGYDVLGNSRG 120

Qy 122 NTWSRRHKTLSDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYFIHSLGTTIGFV 181
Db 121 NTWARRNLYSPDSVEFWAFSDEMAYDLPATIDFIVKTKQKQLHVLVGHVSQGTIGFI 180

Qy 182 AFTSMPELAQRKKNFALGPISFKYPTGIFTRELLPNSLIKAVEGPKGFLEDDKTKI 241
Db 181 AFTSNPSLAKRIKFIYALPATAVTKYKSLINKLRFVQSLFKIFGDKIYFPHNFFDQF 240

Qy 242 ASTKICNNKILWLCSEFMSLWAGSNKNNMQSDMVYMSHAPTGGSSVHNLILKQLVHS 301
Db 241 LATEVCSREMLNLLCSNALFIICGFDKSNFTSLRDVYLSHNPAGTSVQNNFHWTAQVKS 300

Qy 302 DEFRAIDMGNDADNMKNHNSQHPPIYDLTAMKVPTAIWAGHDVILGTPQDVARILPQTKS 361
Db 301 GKFOAYDWGSPQVRMHYDQSPPYVNTAMNVPIAVNNGKDLIADPDQVGLLLPLKPN 360

Qy 362 LSLVLSLLEPEPTDFVWGLDAPQRFES 390
Db 361 L-IYHKEIPFYN-HLDFIWMADAPQEVYN 387

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RESULT 3
LIPG CANFA STANDARD; PRT; 398 AA.
AC P80035; 002857;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) (Gastric
DN lipase) (GL).
GN LIPF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Vaganay S., Joliff G., Bertaux O., Toselli E., Devignes M.D.,
RA Benicourt C.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 20-59.
RX MEDLINE=92037652; PubMed=1935982;
RA Carriere F., Moreau H., Raphael V., Laugier R., Benicourt C.,
RA Junien J.-L., Verger R.;
RT "Purification and biochemical characterization of dog gastric
RT lipase."
RL Eur. J. Biochem. 202:75-83(1991).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y13899; CAA74198.1; -;
DR PIR; S19539; S19539.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 398 TRIACYLGLYCEROL LIPASE, GASTRIC.
FT ACT_SITE 172 172 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 372 372 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 39 39 I -> T (IN REF. 2).
SQ SEQUENCE 398 AA; 45130 MW; E04D62F7518E386C CRC64;

Query Match 48.2%; Score 1031; DB 1; Length 398;
Best Local Similarity 48.8%; Pred. No. 3.1e-77;
Matches 190; Conservative 72; Mismatches 125; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGLTLAGGFLDLENEVNPVMMTSEIIINGYPSEYEVTTEDGYILL 61
Db 1 MWLLTASVLSLTGTTGLGFKLHPTPEVTMISQMTITWGPNEEYEVTTEDGYILG 60

Qy 62 VNRIPIGTRHARSTGRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
Db 61 IDRIPIGKNSGNTGRPRVAFQGLLASATNWSLNPLNNSLAFLADAGYDVLGNSRG 120

Qy 122 NTWSRRHKTLSDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYFIHSLGTTIGFV 181
Db 122 NTWSRRHKTLSDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYFIHSLGTTIGFV 181

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Db 121 NTWARNLYSPDSVEFWAFSEDEMAKYDLPATIDFILKKTQDQLHYVGHSGQTIGFI 180
Qy 182 AFSTPELAQRKMFALGPTISFYKPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 181 AFSTNPKLAKRTYALAPVATVYKTELLNKLMLVPSFLEKLFNGKIFPHHFFDOF 240
Qy 242 ASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNHILHIKOLYS 301
Db 241 LATEVCSRETVLLCSNALFICGFTMNLNLSRLDVLVLSHNPAGTSSVQNLHWSQAVKS 300
Qy 302 DEFRAVDCNDADNKKHYNQSHPPYDILTKAMKVPYTAIWAGGHVGLTPODVARIILPOIKS 361
Db 301 GRQAFDQSPVQNMHHYQSHPPYNTDMHVPYAVWNGNDLLADPHDVLKLLSKLPN 360
Qy 362 LSLVLSLLPEWEPTDFVWGLDAPQRMFS 390
Db 361 L-IYHRKIPPYN-HLDFIWMADPAQAVYN 387

RESULT 4
LIPG_RAT STANDARD; PRT; 395 AA.
AC P04634;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Triacylglycerol lipase, lingual precursor (EC 3.1.1.3) (Lingual
DE lipase).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85215987; PubMed=3839077;
RA Doeherty A.J.P., Bodmer M.W., Angel S., Verger R., Riviere C.,
RA Lowe P.A., Lyons A., Emcage J.S., Harris T.J.R.;
RT "Molecular cloning and nucleotide sequence of rat lingual lipase
RT cDNA."
RL Nucleic Acids Res. 13:1891-1903(1985).
CC -|- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -|- MISCELLANEOUS: LINGUAL LIPASE IS SECRETED BY THE SEROUS (VON
CC EBNER'S) GLANDS AT THE BACK OF THE RAT TONGUE.
CC -|- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC
CC EMBL; X02309; CAA26179.1; -.
CC DR EMBL; A01157; CAA00136.1; -.
CC DR PIR; A23045; LIRTT.
CC DR InterPro; IPR000073; Abhydrolase.
CC DR InterPro; IPR000734; Lipase.
CC DR InterPro; IPR000379; Ser_estrs_site.
CC DR Pfam; PF00561; abhydrolase; 1.
CC DR PROSITE; PS00120; LIPASE_SER; 1.
CC KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
CC FT SIGNAL 1 18
CC FT CHAIN 19 395 TRIACYLGLYCEROL LIPASE, LINGUAL.
CC FT ACT_SITE 171 171 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 342 342 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 371 371 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT DISULFID 245 254 BY SIMILARITY.
CC FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ SEQUENCE 395 AA; 44588 MW; E601854A923522EA CRC64;
Query Match 47.8%; Score 1022.5; DB 1; Length 395;
Best Local Similarity 48.4%; Pred. No. 1.5e-76;
Matches 192; Conservative 67; Mismatches 119; Indels 19; Gaps 3;

Qy 2 MWLLLTTLTCL-----ICGTLNAGGFLDLENENVPVMMNTSEIIIVNGYPSBEYEV 53
Db 1 MWLLLTISVITFGGAHGLFGKLGPG-----NPEANMNIISOMITYWGYPCOEYEV 51
Qy 54 TEDGQVILLVNRTPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYD 113
Db 52 TEDGQVILGYIRPHGKNNSENIGKRPVYVLQHLGLASATNWIANLPNNLSLAFMLADAGYD 111
Qy 114 VMNGSRGNTWSRRHKTLSSETDEKFWAFSEFDEMAKYDLPVDFIVNKTQGEKLYFIGH 173
Db 112 VWLGNRGNTWSRKNNVYSPDSVEFWAFSEFDEMAKYDLPATINFIQVKTQGEKIHVGH 171
Qy 174 LGTTIGFVAFSTMPELAQRKMFALGPTISFYKPTGIFTRFLLPNSIIKAVFGTKGFF 233
Db 172 QGTTIGFIAFSTNPTLAKKIKTFYALAPVATVYKTSQSPKLSIFPTFLFKLMFGKMKPL 231
Qy 234 LEDKTKIASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNHIL 293
Db 232 PHTYFDDFLGTEVCSREVDLLCSNTLFIKCGFDKKNLNVSRFDVYLGHNPAGTSVQDFL 291
Qy 294 HIKOLYHSDFRAYDGNADNKKHYNQSHPPYDILTKAMKVPYTAIWAGGHVGLTPODVA 353
Db 292 HWAQLVRSCKFOAFNWSGSPSQNNLHYNQKTPPEYDVSAMTVFVAVWNGNDILADPDVA 351
Qy 354 RILPOIKSLVLSLLPEWEPTDFVWGLDAPQRMFS 390
Db 352 MLLPKLSNLLPHKKEILA--YNHLDFIWMADPAQEVYN 386

RESULT 5
LICH_RAT STANDARD; PRT; 397 AA.
AC Q64194;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lysosomal acid lipase/cholesteryl ester hydrolase precursor
DE (EC 3.1.1.13) (LAL) (Acid cholesteryl ester hydrolase) (Sterol
DE esterase) (Lipase A) (Cholesteryl esterase).
GN LIPA OR LAL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=96129534; PubMed=8576647;
RA Nakagawa H., Matsubara S., Kuriyama M., Yoshidome H., Fujiyama J.,
RA Yoshida H., Osame M.;
RT "Cloning of rat lysosomal acid lipase cDNA and identification of the
RT mutation in the rat model of Wolman's disease.";
RL J. Lipid Res. 36:2212-2218(1995).
CC -|- FUNCTION: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL
CC ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTOR-
CC MEDIATED ENDOCYTOSIS OF LIPOPROTEIN PARTICLES. IMPORTANT IN
CC MEDIATING THE EFFECT OF LDL (LOW DENSITY LIPOPROTEIN) UPTAKE ON
CC SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION
CC OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION (By
CC similarity).
CC -|- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC acid.
CC -|- SUBCELLULAR LOCATION: Lysosomal.
CC -|- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC
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EMBL; S81497; AAB36043.2; -
InterPro: IPR000073; Abhydrolase.
InterPro: IPR000734; Lipase.
InterPro: IPR000379; Ser_estrs_site.
Pfam: PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; FALSE_NEG.
Hydrolase; Lipid degradation; Glycoprotein; Signal; Lysosome.
FT SIGNAL 1 19
FT CHAIN 20 397
FT ACT_SITE 172 372
FT ACT_SITE 372 372
FT CARBOHYD 34 34
FT CARBOHYD 99 99
FT CARBOHYD 159 159
FT CARBOHYD 271 271
FT CARBOHYD 319 319
FT CARBOHYD 397 397
FT SEQUENCE 397 AA; 45186 MW; 97A38595A0523947 CRC64;

Query Match 47.5%; Score 1015; DB 1; Length 397;
Best Local Similarity 49.1%; Pred. No. 6.3e-76;
Matches 192; Conservative 76; Mismatches 117; Indels 6; Gaps 4;

Qy 2 MWLLTTTCLICGTLNAGGFLDLENEVPMVMTSEIIIVNGYPSSEYVETEDGYILL 61
Db 1 MQLLRVICFVVGILLSGPTTISAVDPEANMNVTEIIMHWGYP--EHSVQTGDGYILG 58
Qy 62 VNRIPIYGRTHARSGPRPVYMQ--HALFADNAYWLENYANGSLGFLADAGYDVMWGS 119
Db 59 VHRIPHGRKKNQFDGKPGPVVYQWHLGFLADSSNVNIDNNSLGFILADAGFDVMWGS 118
Qy 120 RGNTWSRRHKTLSDEKFWAFSDEMAKYDLPVDFIVNKTQOEKLYFGHSLGTTIG 179
Db 119 RGNTWSRRHKTLSVQDEYFAFDEMAKYDLPASINVLNKTQOEQLYNGHSGQTIG 178
Qy 180 FVASTWPELAQRKIMFALGPTISFYPTGIFTRFLLPNSIIKAVFGTKGFLEDKKT 239
Db 179 FIAFSOMPELAKVKMFALAPVLSLNFASGPMVKGLRPLDLLLEDLFGQKFLPQSAMV 238
Qy 240 KIASTKCNKILWLCSEFMSLWAGSKKNMNSRMDVMYSHAPTSSVNIHLIKOLY 299
Db 239 KWLSTHICTHVMKELCANIEFLICGNEKNLNSRVDVYTHCPAGTSVQNMVHWQTV 298
Qy 300 HSDEFAYDNGNDADNMKNHYNOSHPIYDLTAMKVPTAIMAGGHVDVLGTPQDVARILPQI 359
Db 299 KYHKLQAFDWSGSKNYFHYNQSYPLYSIKDMQLPTALWSSGKDLADTSDINILLTEI 358
Qy 360 KSLSLVLSLLPEWETPFDVWGLDAPQRMFS 390
Db 359 PTL-VYHKNIPEWD-HLDFIWGLDAPWRLYN 387

RESULT 6
ID LPC_BOVIN STANDARD; PRT; 397 AA.
AC Q29458;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Triacylglycerol lipase, pregastric precursor (EC 3.1.1.3) (Pregastric lipase) (GL) (Pregastric esterase) (PGE).
GN Lipf.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

RN SEQUENCE FROM N.A.
RC TISSUP-Tongue serous gland;
RX MEDLINE-95011625; PubMed-7926811;
RA Timmermans M.J., Kupers L.P., Teuchy H.;
RT "The cDNA sequence encoding bovine pregastric esterase";
RL Gene 147:259-262(1994).
CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a fatty acid anion.
CC -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC

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EMBL; L26319; AAA57037.1; -
InterPro: IPR000073; Abhydrolase.
InterPro: IPR000734; Lipase.
InterPro: IPR000379; Ser_estrs_site.
Pfam: PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 397
FT ACT_SITE 171 171
FT ACT_SITE 371 371
FT CARBOHYD 33 33
FT CARBOHYD 270 270
FT CARBOHYD 326 326
FT SEQUENCE 397 AA; 45231 MW; F68977DED58EE36 CRC64;

Query Match 46.0%; Score 982.5; DB 1; Length 397;
Best Local Similarity 47.3%; Pred. No. 2.9e-73;
Matches 184; Conservative 72; Mismatches 130; Indels 3; Gaps 3;

Qy 2 MWLLTTTCLICGTLNAGGFLDLENEVPMVMTSEIIIVNGYPSSEYVETEDGYILL 61
Db 1 MWLLTVTCFTHMSGNAFCFLG-KIAKNPEASMNVSQMSIYWGYPSEMHKVVITADGYILQ 59
Qy 62 VNRIPIYGRTHARSGPRPVYMQWALFADNAYWLENYANGSLGFLADAGYDVMWGSRG 121
Db 60 VYRIPHCKNNHNLGQRPVFLQHLGSLGATNLSNLPKNSLGLADAGYDVLGNSRG 119
Qy 122 NTSRRHKTLSDEKFWAFSDEMAKYDLPVDFIVNKTQOEKLYFGHSLGTTIGV 181
Db 120 NTAQEHLYYSPDSPEWAFSDEMAEYDLPSTIDFILLRTGQKKLVHVGHSQGTIGFI 179
Qy 182 AFSWPELAQRKIMFALGPTISFYPTGIFTRFLLPNSIIKAVFGTKGFLEDKKTKI 241
Db 180 AFSPTSLAEKIKVYFALAPVATVKYTSKLNKALIPHLFKIIFGDKMFPHTFLQOF 239
Qy 242 ASTKICNKKILWLCSEFMSLWAGSKKNMNSRMDVMYSHAPTSSVNIHLIKOLXHS 301
Db 240 LGVMSRETLDVLCCKNALFAITGVDNKNFMSRLDVIHNPACTSVQNTLHWQAVKS 299
Qy 302 DEFAYDNGNDADNMKNHYNOSHPIYDLTAMKVPTAIMAGGHVDVLGTPQDVARILPQKS 361
Db 300 GKFOAFOWGAPYQNLHMYHQPPTPIYNTAMNVPYAVWSADNLLADPDQDVFLLSLSN 359
Qy 362 LSLVLSLLPEWETPFDVWGLDAPQRMFS 390
Db 360 L-IYHKEIPNPN-HLDFIWAMDAPQEVYN 386

RESULT 7
ID LICH_MOUSE STANDARD; PRT; 397 AA.
AC Q9Z0M5;
DT 15-JUN-2002 (Rel. 41, Created)

Db	73	GKGRPVVYLQHGELLADSSNNWVTINDNSUGLLEADRGDFVWNGSRGNTWSLKHKTUSV	132
QY	134	TDSEKWFASFDEMAKYDLPCGVIDFVINKTGQERKLYFIGHSLGTTIGFVAFSTMPELAORI	193
Db	133	SQDEFWAFSDEMAKYDLPASINYLKNGQEQIYVGHSGQCTIGFIAFSOMPELAKKI	192
QY	194	KMNFALGPTISFYKPYGTGIFTRFFELPNSIIKAVGFKGFFLEKDKTKTASTKICNNKILM	253
Db	193	KMFLVLAPVLSLNFASGPLLQLGLRPLDKMFQKQKFLPQSAMLKWLSIHVCTHVIMK	252
QY	254	LICSEWLSWAGSNKKNMVQSRMDVYMSHAPYGTSSVHNTHLHKOLYHSDEFPRAYDWGDA	313
Db	253	ELCANVFFLLCGFNEKLNMSRVDDVYTHCPAELLVQNNMLHRGQVFKYKKLQAFDWSSE	312
QY	314	DNKHKYNOSHPPYDYLTAHKVPTAIWAGGHDVLGTPOQVARILTPKITSLSLSVLSLLPWE	373
Db	313	KNTFHYNQSPPSYNTKNNRPLTALWSGGRWLADINDITILLTQIPKL-VYHKNIPEWD	371
QY	374	PTDFVWGLDAPORMF 389	
Db	372	-HLDFIWLGDAPWKLY 386	
RESULT 8			
LIP3_DROME			
ID	LIP3_DROME	STANDARD;	PRT; 394 AA.
AC	O46108;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Lipase 3 precursor (EC 3.1.1.-)		
GN	LIP3 OR CG8823.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;		
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;		
OC	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
ON	NCBI_TaxID=7227;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Canton S;		
RC	STRAIN=Berkeley;		
RC	STRAIN=20196006; PubMed=10731132;		
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA	Abrial J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Fosler C., Gabrielian A.E., Garly N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		

RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- TISSUE SPECIFICITY: FAT BODY.
CC -!- DEVELOPMENTAL STAGE: ONLY AT LARVAL STAGES.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.). ALSO SIMILAR TO
CC LEPIDOPTERAN EGG-SPECIFIC AND YOLK PROTEINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y14367; CAA74737.1; -.
DR EMBL: AE030699; AAF54935.1; -.
DR FlyBase: FBgn023495; Lip3.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000379; Ser.estrs_site.
DR Pfam: PF00561; abhydrolase_1.
DR PROSITE: PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Signal; glycoprotein.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 394 LIPASE 3.
FT ACT_SITE 164 164 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 369 369 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 394 AA; 44901 MW; A/18D1D/43673802 CRC64;
Query Match 24.9%; Score 533; DB 1; Length 394;
Best Local Similarity 33.4%; Pred. No. 2.2e-36;
Matches 118; Conservative 77; Mismatches 148; Indels 10; Gaps 8;
Qy 43 NGYSPSEYVETDGYILLVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGS 102
Db 35 DGYPMERHEVYTSNYYILTMHRIPYSPKGTSSN-RPVAFLMHGMLSSSDWLMGPERS 93
Qy 103 LGFLLADAGYDVWVNSRGNTWSSRRHKLSTDETFKFAFSEDEWAKYDLPGVDFIVNKT 162
Db 94 LAYMLADAGYDVWVNGNRGNTYSKAHKYPTWYQIFWVNFNSMETGMVDYPMADIVYLAKT 153
Qy 163 QGEKLYFTGHSGLTGTVAFSTMPLELAQRKIMNFALQPTI---SFKYP-TGIFTRFPFL 218
Db 154 GOQVQVYVGHSGQITVYLVYVSEPEYNDKLSAHLGLPAAYMGNMKSPLTRAPAPILGO 213
Qy 219 PMSIKAVFGTKGFLEDDKTKYIASTKICNNKILWL-ICSEFMSLWAGSNKKNNQSRMD 277
Db 214 PNAIVE-VCGSMEEFMSNKKFQDLGEMCQATSPYADMCANEIFLGGYDTEQLDYELLE 272
Qy 278 VYMSHAPGSSVHNLHLKQLYHSDPEFRAYDNGDADNKKHYNOSHPPIYDLTAMKVPTA 337
Db 273 HIKATSPAGASVQNLHFCQYNSGKFRKFDY-TALRNPYEGYGFPPDYKLNKAPVL 331
Qy 338 IWAGGHVDLGPQDVARILTPKISLQ-VLSLLPEWETDFVNGLDAPQRMF 389
Db 332 LYYGANDWMCVDSVRKLRDELNPALDYLVPFEKW-AHLDFIWGTARKYVY 383

----- RESULT 9 -----
LIPL_DROME STANDARD; PRT; 439 AA.
ID LIPL_DROME Q9VQR6;
AC 046107; Q9VQR6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-JUN-2002 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lipase 1 precursor (EC 3.1.1.-).
GN LIPL OR C57279.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE OF 7-433 FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=98227315; PubMed=9566193;
RA "The Drosophila melanogaster lipase homologs: a gene family with
RT tissue and developmental specific expression."
RL J. Mol. Biol. 276:877-885(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Branton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flooker C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: COULD BE A DIGESTIVE ENZYME.
CC -!- TISSUE SPECIFICITY: OVARIES.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.). ALSO SIMILAR TO
CC LEPIDOPTERAN EGG-SPECIFIC AND YOLK PROTEINS.
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DR EMBL; Y14366; CAA74736.1; -;
DR EMBL; AE003629; AAF52994.1; -;
DR FlyBase; FBgn0023496; Lip1.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; FALSE_NEG.
KW Hydrolyase; Lipid degradation; Signal; Glycoprotein.
FT SIGNAL 1 24
FT CHAIN 25 439
FT DOMAIN 30 44
FT ACT_SITE 197 197
FT ACT_SITE 393 393
FT CARBOHYD 124 124
FT CARBOHYD 151 151
FT CARBOHYD 346 346
FT CARBOHYD 379 379
FT CARBOHYD 426 426
FT CONFLICT 10 10
FT CONFLICT 213 213
FT CONFLICT 412 412
SQ SEQUENCE 439 AA; 50660 MW; 9E3E20BEAE93E3F CRC64;

Query Match 22.7%; Score 486; DB 1; Length 439;
Best Local Similarity 30.1%; Pred. No. 1.8e-32;
Matches 127; Conservative 71; Mismatches 170; Indels 54; Gaps 10;

QY 1 MWLLLTTCCLICGTLNA---GGFLDLENE-----VNPVVM 34
DB 7 MQLLLGLCVFISRIQOLIGGEDEDEDEEEESVEDETPEDRLQRKNIKQDSTL 66
QY 35 NTSEIIYNGYPSEYEYVTTEDGYILLVNRIPYGRTHARSTGPRPVVYMQHALFADNAYW 94
DB 67 SVDKLIAYGYESEVHHVTTEDGYILLTHRI-----RKQAPPFL-LQHLGVDSAGF 118
QY 95 LENYANGSLGFLADAGYDVMGNSRGNTWSRRHKTSETDEKFWAFSEDEMAKYDLPGV 154
DB 119 VVMGPNVSLAYLLADHNTDVLGNARGNRYSRNHTTLPDDESKFWDFSWHEIGMYDLPAM 178
QY 155 IDFIYVNTQKLYFTGHSGLTTCGFVAFSTMPPELAQRKMNFAFGPTISEK-----YP 208
DB 179 IDHVLKVTGFPKLHAGHSQGCSTFFVCMSPAYNDKVMQALAPAVYAKETEDHPYI 238
QY 209 TGIFTRFLLPNSIIKAVFGTKGFFLEDKTKTKIASTKICNNKILICSEFMSLWAGSNK 268
DB 239 RAISLYFNSLVGSSIREMFENGFEFL--CRMTEETERLCIEAVFGIV-----GRNW 287
QY 269 KNNQSRMDVYMSHAPTGSVVNIHLIKQLYHSDFRAYDNGNDADNKKHYNSHPIPYD 328
DB 288 NEFNKMFPEVILGHYPAGVAAKQVAFHFIQIKSGRFAPYSYSSN-KNMQLYRDLPLPPRYN 346
QY 329 LFAMKVPATWAGGHVLTGTPQDVARILPQIKSLSLVLSLPEWE-PTFDFFVWGLDAPQR 387
DB 347 LSLVTPVTFVYYSTNDLCHPKDVESMDDLGNTV-GKYLVPQKEFNHMDFLWADVRKM 405
QY 388 MF 389
DB 406 LY 407

RESULT 10
TGLL_YEAST
ID TGLL_YEAST STANDARD; PRT; 548 AA.
AC P34163;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Triglyceride lipase-cholesterol esterase (EC 3.1.1.-).
GN TGL1 OR YKL140W OR YKL5.
OS Saccharomycetes cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92245761; PubMed=1574929;
RA Abraham P.R., Mulder A., Van't Riet J., Planta R.J., Raue H.A.;
RT "Molecular cloning and physical analysis of an 8.2 kb segment of
RT chromosome XI of Saccharomycetes cerevisiae reveals five tightly linked
RT genes.";
RL Yeast 8:227-238(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Rad M.R., Xu G., Kirchrath L., Fritz C., Keuchel H., Hollenberg C.P.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
GC -!- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY.
CC -----
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CC -----
DR EMBL; Z25464; CAA80958.1; -;
DR EMBL; Z28140; CAA81981.1; -;
DR PIR; S37969; S37969.
DR PIR; S39000; S39000.
DR SGD; S0001623; TGL1.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
KW Hydrolyase; Lipid degradation.
SQ SEQUENCE 548 AA; 62979 MW; 32D1F230701CB083 CRC64;

Query Match 16.0%; Score 342.5; DB 1; Length 548;
Best Local Similarity 29.6%; Pred. No. 1.4e-20;
Matches 107; Conservative 63; Mismatches 133; Indels 59; Gaps 13;

QY 48 EEEYVTTEDGYILLVNRIPYGRTHARSTGPRPVVYMQHALFADNAYW---LENYANGSLG 104
DB 78 EDHLVRTEDNYLTLRIP---PISKRNFNKVVYLHGLLMCSDVWCNIEHRKN--LP 132
QY 105 FLLADAGYDVMGNSRGNTWSRRHKTSETDEKFWAFSEDEMAKYDLPGVIDFVNTGQ 164
DB 133 FVLHDLGYDVMGNNRGNKYSTAHLNKKPKSNKFWDFSIDEFAFFDIPNSIEFILDITKV 192
QY 165 EKLFIHSLGTTIGFVAFSTMPPELAQRKMNFAFGPTISFKYPTGIFTRFLLPNSIIF 224
DB 193 DKVICIGFSQSAQAFSAFSEKLNKRVSHFIALAPMT---PKGLHNR---IVDTLAK 246
QY 225 AVFGTKGFFLEDKTKTKIASTKICN-----NKLWLCSEFMSLWAGSNKK 269
DB 247 SSPGPMFLFF-GRKIVLPASVIVQRTLTHTLFLNCLIDIANKILF-----NWK 292
QY 270 NNNQSRMDVYMSHAP--TGSSVHNILHLIKQLYHSDFRAYDNGNDADNKK---KHYNOS 322
DB 293 SFNLPKROKIASYAKLYSTTSVKSVHWFQILRSQKQFOMFE---ESDNLNLSLRPYQIA 349
QY 323 HPPIYDLTAMKVPATWAGGHVLTGTPQDVARILPQIKSLSLVLSLPEWEPTFDFFVWGL 382
DB 350 NFP--TRTNKIPILLIYGGIDSLVIDVMKNLP-----FNSVFDVKVDNYEHLDLNGK 403
QY 383 DA 384
DB 404 DA 405

[illegible]

Db	512	MLL--RVLVESDAKELNKRIVYETMYTAALENSVDLQSPYSGSPGQAIL----	Q	565
QY	112	YDVMGNSRGNTWSRRHKLTSETDEKFWAFSFDMAKYDLPGVIDFVNKTGOEKLYFIG	171	
Db	566	FDWVN-----AKVDNKYW--DWDE-----LKLKIATKGLRNLILL--	598	
QY	172	HSLGTTIGFVAFSTMPELAQRKMKNFALGPTISFK-YPTGIFTR-----FFLLPNSIHK	224	
Db	599	-----APMETAS-----TSQILGNNSFEFPTSNIIYRVLVSGEFFVYNPHLLK	642	
QY	225	AVFTKGFLEDKTKTIASKIKCNN-----KILWLSCSEFMSLWAGSN	267	
Db	643	DLF-DRLGWDMDKQQL-----IAHNGSIQVISEIPDDLKELYKTWFKOKNIIDMAADR	697	
QY	268	KKNMNQSR-MDVYMSHAPTG---SSVH	290	
Db	698	GYFDQSQSLNIYI-QKPTFAKLSSMH	723	
RESULT 15				
BPHD_PSES1				
ID	BPHD_PSES1	STANDARD;	PRT;	277 AA.
AC	PI7548;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1.-).			
GN	BPHD.			
OS	Pseudomonas sp. (strain KKS102).			
OC	Bacteria; Proteobacteria.			
OX	NCBI_TaxID=307;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89213965; PubMed=2540155;			
RA	Kimbara K., Hashimoto T., Fukuda M., Koana T., Takagi M., Oishi M.,			
RA	Yano K.;			
RT	"Cloning and sequencing of two tandem genes involved in degradation			
RT	of 2,3-dihydroxybiphenyl to benzoic acid in the polychlorinated			
RT	biphenyl-degrading soil bacterium Pseudomonas sp. strain KKS102.;"			
RL	J. Bacteriol. 171:2740-2747(1989).			
CC	-1- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS			
CC	(PCB) TO BENZOIC ACID AND CHLOROBENZOIC ACIDS.			
CC	-1- SIMILARITY: STRONG, TO E.COLI MHPC.			
CC				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/anno			
CC	or send an email to license@isb-sib.ch).			
CC				
CC	EMBL; M26433; AAA25751.1; -			
DR	PIR; B32312; ESPSSK.			
DR	InterPro; IPR0031089; AB_hydrolase.			
DR	InterPro; IPR000073; Abhydrolase.			
DR	InterPro; IPR000379; Ser_estr_site.			
DR	Pfam; PF00561; abhydrolase; 1.			
DR	PRINTS; PR00111; ABHYDROLASE.			
KW	Aromatic hydrocarbons catabolism; Hydrolase.			
FT	ACT_SITE 112 112 BY SIMILARITY.			
SEQUENCE	277 AA; 30253 MW; E0C7496186818D1E CRC64;			
Query Match 4.5%; Score 97; DB 1; Length 277;				
Best Local Similarity 20.5%; Pred. No. 0.84;				
Matches 68; Conservative 39; Mismatches 111; Indels 114; Gaps				
QY	69	RTHARSTGPRPVVYMOHALFADNAYLWENYANGSLGFLLDACGYDVMGNSRGNTWSRRH	128	
Db	24	RHLNDAGQGERVIMLHGFGGAGGWSNYRNN--IG-PFVEAGYRLLPDAPG-----	73	
QY	129	KTLSSETDEKEWAFSDFD-----MAKYDLPGVIDFVNKTGOEKLYFIGHSLGTTIGVAFS	184	

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Db 74 ---FNKSD---TVVMDQRLVNARSVKGMMDVL-----GIERKAHLVGNMSG---GAGALN 120
QY 185 TWPDLAQRIKMNFFALGPTTISEKYPTCIFTREF-LLPNSIIKAVFGTKGFFLEDKKTIAS 243
Db 121 FALEYPERTGKILMG-----PGLGNSLFTAMPMEGIKLLF----- 157
QY 244 TKICNNKILWLICSEFMSLWAGSNKKNNMQSRMDVYMSHAPTGSSVHNILHIKQLYHSDE 303
Db 158 -----KLYAEPSELETKQ-----MLNVFLFDQSVITDE 185
QY 304 FRAYDGNADNNKHYNQSHPIYDLTAMKYPTAIWAGGHDVLGTPQDVARILPOIKSLS 363
Db 186 LLQGRWANTORNPEHLKN-----FILSAOKVPLSAW-----DVSARLGEIKAKT 229
QY 364 LVLSLLPEWEPTDFVWGLDAPQRMFSGNNHL 395
Db 230 LV-----TWGRD--DRFVPLDHGL 246
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Search completed: April 2, 2003, 16:41:25
Job time : 24 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:38:33 ; Search time 94 Seconds
(without alignments)
865.836 Million cell updates/sec

Title: US-10-003-302-2.

Perfect score: 2137

Sequence: 1 MMWLLTTTLCIGTLNAGG.....FDFVGLDAPQRMFSGNHL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1059.5	49.6	395	11 Q9D798	Q9D798 mus musculus
2	1058.5	49.5	395	11 Q9D6T5	Q9D6T5 mus musculus
3	1057.5	49.5	395	11 Q9C2P7	Q9C2P7 mus musculus
4	1056.5	49.4	395	11 Q9D6Q6	Q9D6Q6 mus musculus
5	1056.5	49.4	395	11 Q9D6P3	Q9D6P3 mus musculus
6	1055.5	49.4	395	11 Q9D6X0	Q9D6X0 mus musculus
7	1055.5	49.4	395	11 Q9D6L9	Q9D6L9 mus musculus
8	1053.5	49.3	395	11 Q9D7C5	Q9D7C5 mus musculus
9	1052.5	49.3	395	11 Q9D767	Q9D767 mus musculus
10	1050.5	49.2	395	11 Q9C2P8	Q9C2P8 mus musculus
11	1049.5	49.1	395	11 Q9D760	Q9D760 mus musculus
12	1048.5	49.1	395	11 Q9D766	Q9D766 mus musculus
13	1048.5	49.1	395	11 Q9D6S5	Q9D6S5 mus musculus
14	1046.5	49.0	395	11 Q9D796	Q9D796 mus musculus
15	1045.5	48.9	395	11 Q9D6Q3	Q9D6Q3 mus musculus
16	1045.5	48.9	395	11 Q9D6N8	Q9D6N8 mus musculus

17	1045.5	48.9	395	11	Q9D6L1	Q9D6L1 mus musculus
18	1043.5	48.8	395	11	Q9D6M9	Q9D6M9 mus musculus
19	1040.5	48.7	395	11	Q9D6Q2	Q9D6Q2 mus musculus
20	995	46.6	374	4	Q96LG2	Q96LG2 homo sapien
21	663.5	31.0	405	5	Q93789	Q93789 caenorhabdi
22	649	30.4	181	11	Q9D7R3	Q9D7R3 mus musculus
23	644.5	30.2	403	5	Q61866	Q61866 caenorhabdi
24	641.5	30.0	684	5	Q95XV1	Q95XV1 caenorhabdi
25	634	29.7	411	5	Q20449	Q20449 caenorhabdi
26	623.5	29.2	404	5	Q16956	Q16956 caenorhabdi
27	585.5	27.4	411	5	Q94252	Q94252 caenorhabdi
28	574.5	26.9	351	5	Q95X33	Q95X33 caenorhabdi
29	561.5	26.3	399	5	Q9VPE9	Q9VPE9 drosophila
30	548.5	25.7	434	5	Q9VKT9	Q9VKT9 drosophila
31	546.5	25.6	426	5	Q17766	Q17766 caenorhabdi
32	546	25.5	456	5	Q9VK55	Q9VK55 drosophila
33	542.5	25.4	398	5	Q9V796	Q9V796 drosophila
34	511.5	23.9	416	5	Q9VQ05	Q9VQ05 drosophila
35	511	23.9	616	5	Q77107	Q77107 plodia inte
36	508	23.8	457	5	Q9VKT2	Q9VKT2 drosophila
37	508	23.8	457	5	Q8T3X7	Q8T3X7 drosophila
38	502.5	23.5	559	5	Q17219	Q17219 bombyx mori
39	495	23.2	435	5	Q9VG46	Q9VG46 drosophila
40	482.5	22.6	838	5	Q9VVK6	Q9VVK6 drosophila
41	477	22.3	406	5	Q9VKT7	Q9VKT7 drosophila
42	469.5	22.0	401	5	Q9U276	Q9U276 caenorhabdi
43	445.5	20.8	457	5	Q95U37	Q95U37 drosophila
44	437	20.4	169	11	Q9D2L7	Q9D2L7 mus musculus
45	436	20.4	443	3	P78898	P78898 schizosacch

ALIGNMENTS

RESULT 1

Q9D798	PRELIMINARY;	PRT;	395 AA.
ID	Q9D798		
AC	Q9D798;		
DT	01-JUN-2001 (TREMBlrel. 17, Created)		
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)		
DT	01-MAR-2002 (TREMBlrel. 20, Last annotation update)		
DE	2310051B21RIK protein.		
GN	2310051B21RIK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=TONGUE;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
DR	EMBL; AK009431; BAB26283.1; -;		
DR	MGI; MGI:1914967; 2310051B21RIK.		

DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00561; abhydrolase; 1.
DR PROSITE: PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44603 MW; 3DFD8B6F6A671E3E CRC64;

Query Match 49.6%; Score 1059.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 3.1e-79;
Matches 196; Conservative 66; Mismatches 124; Indels 3; Gaps 2;

Qy 2 MWLLTTTTCICGTNAGGFLDLENEVNPVWMTSEIIINGYSEYEVTTEDGYILL 61
Db 1 MWLLLVTS-VLSAFGGAHGLFKLGPKNPEANMNYSQMITYWGYPSEYEVTTEDGYILG 59
Qy 62 VNRIPYGTHTARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 60 VYRIPYGNKNSENICKRPVAYLOHGLIASATWITNLPNSLAFILADAGYDVWNGNSRG 119
Qy 122 NWSRRHKTLSDEKFWAFSDEMAKYDLPQVIDFIVNKTQGEKLYFIGHSLGTTIGFV 181
Db 120 NWSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVQKTQGEKIHVYVGHSGTTIGFI 179
Qy 182 AFSTMPELAQRKMFALGPTISFYPTGIFTRFELLSIISIKAVFGTKGFLEDKTKKI 241
Db 180 AFSTNPALAKKIKRYALAPVATVRYTESPKKISLIPKFLKVIFGNKMFPHNYLDQF 239
Qy 242 ASTKCNKILWLICSEFMSLWAGSNKKNMOSRMDVYMSHAPTSSVHNILHIKOLYHS 301
Db 240 LGTEVCSRELLDLCSNALFICFGDKKNLNVSRDLVGHNPAGTSTQDLEFHWLAQLAKS 299
Qy 302 DEFRAIDMGNDADNNKHYNQSHPPYIDLTAMKVPTAIWAGGHVLTGTPQDVARILPQIKS 361
Db 300 GKLOAYNNGSPLONNMLHYNQKTPPYDVSAMTVPITAVWNGGHDILADQDVAMLLPKLPN 359
Qy 362 LSLVLSLPEWEPPTDFWGLDAPORMFS 390
Db 360 LLYHKELP--YNHLDFIWMADPOEVYN 386

RESULT 2

Q9D6T5 ID Q9D6T5 PRELIMINARY; PRT; 395 AA.
AC Q9D6T5;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
clone:2310061A13, full insert sequence.
GN 2310051B2IRIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boftelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Washima J., Mazzarelli J., Wombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sagaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009990; BAB26629.1; -;
DR MGD: MGI:1914967; 2310051B2IRIK.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00561; abhydrolase; 1.
DR PROSITE: PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44623 MW; 3DF96DB83161C3EF CRC64;

Query Match 49.5%; Score 1058.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 3.7e-79;
Matches 196; Conservative 65; Mismatches 125; Indels 3; Gaps 2;

Qy 2 MWLLTTTTCICGTNAGGFLDLENEVNPVWMTSEIIINGYSEYEVTTEDGYILL 61
Db 1 MWLLLVTS-VLSAFGGAHGLFKLGPKNPEANMNYSQMITYWGYPSEYEVTTEDGYILG 59
Qy 62 VNRIPYGTHTARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 60 VYRIPYGNKNSENICKRPVAYLOHGLIASATWITNLPNSLAFILADAGYDVWNGNSRG 119
Qy 122 NWSRRHKTLSDEKFWAFSDEMAKYDLPQVIDFIVNKTQGEKLYFIGHSLGTTIGFV 181
Db 120 NWSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVQKTQGEKIHVYVGHSGTTIGFI 179
Qy 182 AFSTMPELAQRKMFALGPTISFYPTGIFTRFELLSIISIKAVFGTKGFLEDKTKKI 241
Db 180 AFSTNPALAKKIKRYALAPVATVRYTESPKKISLIPKFLKVIFGNKMFPHNYLDQF 239
Qy 242 ASTKCNKILWLICSEFMSLWAGSNKKNMOSRMDVYMSHAPTSSVHNILHIKOLYHS 301
Db 240 LGTEVCSRELLDLCSNALFICFGDKKNLNVSRDLVGHNPAGTSTQDLEFHWLAQLAKS 299
Qy 302 DEFRAIDMGNDADNNKHYNQSHPPYIDLTAMKVPTAIWAGGHVLTGTPQDVARILPQIKS 361
Db 300 GKLOAYNNGSPLONNMLHYNQKTPPYDVSAMTVPITAVWNGGHDILADQDVAMLLPKLPN 359
Qy 362 LSLVLSLPEWEPPTDFWGLDAPORMFS 390
Db 360 LLYHKELP--YNHLDFIWMADPOEVYN 386

RESULT 3

Q9C9P7 ID Q9C9P7 PRELIMINARY; PRT; 395 AA.
AC Q9C9P7;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE 2310051B2IRIK protein.
GN 2310051B2IRIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

```

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001);
DR EMBL; AK010236; BAB26787.1; -
DR EMBL; AK009413; BAB26727.1; -
DR EMBL; AK009428; BAB26280.1; -
DR EMBL; AK009459; BAB26300.1; -
DR EMBL; AK009473; BAB26312.1; -
DR EMBL; AK009474; BAB26313.1; -
DR EMBL; AK009479; BAB26316.1; -
DR EMBL; AK009523; BAB26338.1; -
DR EMBL; AK009525; BAB26339.1; -
DR EMBL; AK009546; BAB26352.1; -
DR EMBL; AK009571; BAB26368.1; -
DR EMBL; AK009573; BAB26370.1; -
DR EMBL; AK009729; BAB26466.1; -
DR EMBL; AK009773; BAB26495.1; -
DR EMBL; AK010019; BAB26647.1; -
DR EMBL; AK010035; BAB26656.1; -
DR EMBL; AK010058; BAB26673.1; -
DR EMBL; AK010061; BAB26675.1; -
DR EMBL; AK010124; BAB26715.1; -
DR EMBL; AK010125; BAB26716.1; -
DR MGD; MGI:1914967; 2310051B21Rik.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44637 MW; D3F96B65EA671E34 CRC64;

Query Match 49.5%; Score 1057.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 4.5e-79;
Matches 196; Conservative 65; Mismatches 125; Indels 3; Gaps 2;

QY 2 MWLLTTTCLICGTLNAGGFLDLENEVNEPVMNTSEIIYNGYPSSEYEVTTEDGYLL 61
DB 1 MWLLLVTS-VLSAFGGAHGLFGKLGPKNPANMNVSMITWGYPSSEYEVTTEDGY 59

QY 62 VNRIYGRTHARSTGPRPVYVMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
DB 60 VIPIYCKKNSENIGKRPVAYLQHLGLASATNWTNLPNNLSAFILADAGYDVMGNSRG 119

QY 122 NTSRRHKLTSETDEKFWAFSFDMAKYDLPVDFIVNKTGOEKLFIHSLGTTIGFV 181
DB 120 NTSRKNNVYSPDSVEFWAFSFDMAKYDLPATIDFIVKTGOEKIHYVHSGQTIGFI 179

QY 182 AFSTMPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGKFFLEDKTKI 241
DB 180 AFSTNPALAKKIKRFYALAPVATVKYTESPKKISLIPKFLKLVFGNKMFMHNYLDQF 239

QY 242 ASTKICNKLWLICSEFMSLWAGSNKKNMNSRMDVYMSHAPGSSVHNLIHLKQLYHS 301
DB 240 LGTEVCSRELLDLCSNALFIFCGFDKKNLNSREDVYLGHNPAAGTSTQDLFWHAQLAKS 299

QY 302 DEFRAWDGNDADNKKHYNSHPPIYDLTAMKVPTAIWAGHDVLTGPQDVARILPOLKS 361
DB 300 GKLOAYNNGSPQLNMLHYNQTPPYDYVSAMTVPVIAVWNGGHDILADPDQVAMLLPKLPN 359

QY 362 LSLVLSLLPEWEPTTFDFVWGLDAPQRMFS 390
DB 360 LLYHKEILP--YNHLDFIWDAPQEVYN 386

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RESULT 4

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Q9D6Q6
ID Q9D6Q6 PRELIMINARY; PRT; 395 AA.
AC Q9D6Q6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:2310067K20, full insert sequence.
GN 2310051B21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010093; BAB26697.1; -
DR MGD; MGI:1914967; 2310051B21Rik.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44623 MW; 245055F5E7FF07C9 CRC64;

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Query Match 49.4%; Score 1056.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 5.5e-79;
Matches 196; Conservative 65; Mismatches 125; Indels 3; Gaps 2;

QY 2 MWLLTTTCLICGTLNAGGFLDLENEVNEPVMNTSEIIYNGYPSSEYEVTTEDGYLL 61
DB 1 MWLLLVTS-VLSAFGGAHGLFGKLGPKNPANMNVSMITWGYPSSEYEVTTEDGY 59

QY 62 VNRIYGRTHARSTGPRPVYVMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
DB 60 VIPIYCKKNSENIGKRPVAYLQHLGLASATNWTNLPNNLSAFILADAGYDVMGNSRG 119

QY 122 NTSRRHKLTSETDEKFWAFSFDMAKYDLPVDFIVNKTGOEKLFIHSLGTTIGFV 181
DB 120 NTSRKNNVYSPDSVEFWAFSFDMAKYDLPATIDFIVKTGOEKIHYVHSGQTIGFI 179

QY 182 AFSTMPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGKFFLEDKTKI 241
DB 180 AFSTNPALAKKIKRFYALAPVATVKYTESPKKISLIPKFLKLVFGNKMFMHNYLDQF 239

QY 242 ASTKICNKLWLICSEFMSLWAGSNKKNMNSRMDVYMSHAPGSSVHNLIHLKQLYHS 301
DB 240 LGTEVCSRELLDLCSNALFIFCGFDKKNLNSREDVYLGHNPAAGTSTQDLFWHAQLAKS 299

QY 302 DEFRAWDGNDADNKKHYNSHPPIYDLTAMKVPTAIWAGHDVLTGPQDVARILPOLKS 361
DB 300 GKLOAYNNGSPQLNMLHYNQTPPYDYVSAMTVPVIAVWNGGHDILADPDQVAMLLPKLPN 359

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Db 120 NTWSRKNVYSPDSVEFWAFSDEMAYDLPATIDFIVQKTGOEKIHYVHSGQTTIGFI 179
Qy 182 AFTSMPELAQRKKNFALGPTISFKYPTGIETRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFSINPALAKKIKRYALAPVATVKYTESPKKISLIPFKLLKVFIGNKMFPHNYLDQF 239
Qy 242 ASTKICNNKILWLICSEPMWSLWAGNKKNNOSRMDVYMSHAPTSSVHNHILHKLQYHS 301
Db 240 LGTEVCSRELLDLCSNLFIFCGFDKKNLVSRFDVVLGHNPAGTSTQDLFHWLAQAKS 299
Qy 302 DEFRAWDGNDADNMKNHYNQSHPPYDITAMKVPTAIWAGGHVLTGTPQDVARILPQKTS 361
Db 300 GKLOAYNMGSPQLNMLHYNQTPPYDVSAMTPIAVWNGGHDILADPDQDVAMLLPKLPN 359
Qy 362 LSLVLSLLPEWEPTDFVWGLDAPQRMES 390
Db 360 LLYHKEILP--YNHLDIFIWAMDAPQEVYN 386

RESULT 7
ID Q9D6L9 PRELIMINARY; PRT; 395 AA.
AC Q9D6L9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
clone:2310076L13, full insert sequence.
GN 2310051B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., King B., Kachiwa H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010203; BAB26766.1; -
DR MGD; MGI:1914967; 2310051B21RIK.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase.1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44671 MW; E8936162510A55C CRC64;

Query Match 49.4%; Score 1055.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 6.6e-79;
Matches 196; Conservative 64; Mismatches 126; Indels 3; Gaps 2;

Qy 2 MWLLTTTCLICGTLNAGGFLDLNENVEVMMNTSEIIIVNGYPSSEYEVTTEDGYLL 61
Db 1 MWLLLVTS-VLSAFGGAGHGLGKLPKNPEANMNVSMQITWGYPSSEYEVTTEDGYLL 59

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Qy 62 VNRIPYGRTHARSTGRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGSRG 121
Db 60 VYRIPYGRKNSNIGKRPVAYLQGLIASATNWTNLPNSLAFILADAGYDVWNGSRG 119
Qy 122 NTWSRHRKTLSETDEKFWAFSDEMAYDLPATIDFIVQKTGOEKIHYVHSGQTTIGFI 181
Db 120 NTWSRKNVYSPDSVEFWAFSDEMAYDLPATIDFIVQKTGOEKIHYVHSGQTTIGFI 179
Qy 182 AFTSMPELAQRKKNFALGPTISFKYPTGIETRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFSINPALAKKIKRYALAPVATVKYTESPKKISLIPFKLLKVFIGNKMFPHNYLDQF 239
Qy 242 ASTKICNNKILWLICSEPMWSLWAGNKKNNOSRMDVYMSHAPTSSVHNHILHKLQYHS 301
Db 240 LGTEVCSRELLDLCSNLFIFCGFDKKNLVSRFDVVLGHNPAGTSTQDLFHWLAQAKS 299
Qy 302 DEFRAWDGNDADNMKNHYNQSHPPYDITAMKVPTAIWAGGHVLTGTPQDVARILPQKTS 361
Db 300 GKLOAYNMGSPQLNMLHYNQTPPYDVSAMTPIAVWNGGHDILADPDQDVAMLLPKLPN 359
Qy 362 LSLVLSLLPEWEPTDFVWGLDAPQRMES 390
Db 360 LLYHKEILP--YNHLDIFIWAMDAPQEVYN 386

RESULT 8
ID Q9D7C5 PRELIMINARY; PRT; 395 AA.
AC Q9D7C5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
GN 2310051B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., King B., Kachiwa H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009359; BAB26240.1; -
DR MGD; MGI:1914967; 2310051B21RIK.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase.1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44748 MW; 3ED43992458DE058 CRC64;

Query Match 49.3%; Score 1053.5; DB 11; Length 395;

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Best Local Similarity 50.1%; Pred. NO. 9.7e-79;
Matches 195; Conservative 65; Mismatches 126; Indels 3; Gaps 2;

QY 2 MWLLTTTTCICGTLNAGFLDLENEVPEVMWNTSEIIINGYPSSEEVTTEDGYILL 61
Db 1 MWLLLVTS-VLSAFGGAHGLFGKLGPKNPEANMNVSMQITWGYPSSEEVTTEDGYILG 59
QY 62 VNRIPIGYTHARSTGRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 60 VYRIPIYGGKNSENICKRPVAYLQHGLIASAKNWIITLNPNSLAFILADAGYDVWNGNSRG 119
QY 122 NTWSRRHKTLSSTDEKFWAFSDEMAKYDLPCGVDFIVNKTQOEKLYFIGHSLGTITGFV 181
Db 120 NTWSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVKTQOEKIHVGHSGQTITGFI 179
QY 182 AFSTWPELAORIKMNFALGPTISEKPYGTGIFTRFLLPNSIIKAVFGTKGPFLEDKTKI 241
Db 180 AFSTNPALAKKIKRYALAPVATVYTESPFKKIIFPKFLKVIKNGMFMFPHNYLDQF 239
QY 242 ASTKCNKILWLCSEFMSLWAGSNKKNMQSRMDVYMSHAPTSSVHNILHIKOLYHS 301
Db 240 LGTECVSRELLDLCSNALFIFCGFDKKNLVSRFVDVVLGHNPAGTSTQDLFHHQAQLAKS 299
QY 302 DEFRAIDGNDADNMKHNQSHPPYIDLTAMKYPTAIWAGGHVDVLTGTPQDVARIILPQKS 361
Db 300 GKLOYNMGSPLOQNLMLHYNQKTPPYIDVSAMTVPYAVWNGGHDILADPQDVAMLLPKLPN 359
QY 362 LSLVLSLPEWEPTDFVWGLDAPORMFS 390
Db 360 LLYHKEILP--YNHLDFTWMDAPQEVYN 386

RESULT 9
Q9D767 PRELIMINARY; PRT; 395 AA.
ID Q9D767 AC Q9C9P8;
AC Q9C9P8;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE 2310051B21RIK protein.
GN 2310051B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuenli P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
DR EMBL; AK009537; BAB26346.1;
DR MGD; MGI:1914967; 2310051B21RIK.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.

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DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44607 MW; E43317C2254FA8FB CRC64;

Query Match 49.3%; Score 1052.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. NO. 1.2e-78;
Matches 195; Conservative 65; Mismatches 126; Indels 3; Gaps 2;

QY 2 MWLLTTTTCICGTLNAGFLDLENEVPEVMWNTSEIIINGYPSSEEVTTEDGYILL 61
Db 1 MWLLLVTS-VLSAFGGAHGLFGKLGPKNPEANMNVSMQITWGYPSSEEVTTEDGYILG 59
QY 62 VNRIPIGYTHARSTGRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 60 VYRIPIYGGKNSENICKRPVAYLQHGLIASAKNWIITLNPNSLAFILADAGYDVWNGNSRG 119
QY 122 NTWSRRHKTLSSTDEKFWAFSDEMAKYDLPCGVDFIVNKTQOEKLYFIGHSLGTITGFV 181
Db 120 NTWSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVKTQOEKIHVGHSGQTITGFI 179
QY 182 AFSTWPELAORIKMNFALGPTISEKPYGTGIFTRFLLPNSIIKAVFGTKGPFLEDKTKI 241
Db 180 AFSTNPALAKKIKRYALAPVATVYTESPFKKIIFPKFLKVIKNGMFMFPHNYLDQF 239
QY 242 ASTKCNKILWLCSEFMSLWAGSNKKNMQSRMDVYMSHAPTSSVHNILHIKOLYHS 301
Db 240 LGTECVSRELLDLCSNALFIFCGFDKKNLVSRFVDVVLGHNPAGTSTQDLFHHQAQLAKS 299
QY 302 DEFRAIDGNDADNMKHNQSHPPYIDLTAMKYPTAIWAGGHVDVLTGTPQDVARIILPQKS 361
Db 300 GKLOYNMGSPLOQNLMLHYNQKTPPYIDVSAMTVPYAVWNGGHDILADPQDVAMLLPKLPN 359
QY 362 LSLVLSLPEWEPTDFVWGLDAPORMFS 390
Db 360 LLYHKEILP--YNHLDFTWMDAPQEVYN 386

RESULT 10
Q9C9P8 PRELIMINARY; PRT; 395 AA.
ID Q9C9P8 AC Q9C9P8;
AC Q9C9P8;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE 2310051B21RIK protein.
GN 2310051B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuenli P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;

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RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010116; BAB26711.1; -.
DR EMBL; AK009300; BAB26201.1; -.
DR MGD; WGI:1914967; 2310051B21Rik.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44579 MW; D2296865EA671D34 CRC64;

Query Match 49.2%; Score 1050.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 1.7e-78;
Matches 195; Conservative 65; Mismatches 126; Indels 3; Gaps 2;

Qy 2 MWLLTTTCLICGTLNAGGFLDLENEVPVMTSEIIYNGYSEYEVTTEDGYILL 61
Db 1 MWLLLVTS-VLSAFGAGHGLFGKLPKPEANMNVSQMITYWGYPSEYEVTTEDGYILG 59
Qy 62 VNRIPIYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMWGNRSR 121
Db 60 VYRIPIYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMWGNRSR 119
Qy 122 NTSRRHKTLSDEKFWAFSDEMAYKDYLPVIDFIVNKTQGEKLYFIGHSLGTTIGFV 181
Db 120 NTSRRKNNVYSPDSVEFWAFSDEMAYKDYLPVIDFIVNKTQGEKLYFIGHSLGTTIGFV 179
Qy 182 AFSTMPALAKIKREYALAPVATVRYTESPFKKISLIPKFLKLVIFGNKMFPHNYLDQF 239
Db 180 AFSTMPALAKIKREYALAPVATVRYTESPFKKISLIPKFLKLVIFGNKMFPHNYLDQF 239
Qy 242 ASTKICNNKILWLICSEFMSLWAGSNKKNQSDVMYSHAPTSVSSVNIHLIKOLYHS 301
Db 240 LGTEVCSRELLDLCSNALIFCGFDKKNLNVRSRGVTLGHNPAGTSTQDLFHWLAQLAKS 299
Qy 302 DEFRAVDGNADNMKNHYNQSHPIYDLTAMKVPYTAIWAGGHDVLTGTPQDVARIILPOIKS 361
Db 300 GKLYANNNGSLQNLMLHYNQKTPPYDVSAMTVPYAVWNGGHDILADPDQVAMLLPKLPN 359
Qy 362 LSLVLSLPEWPTDFVWGLDAPORMFS 390
Db 360 LLYHKEILP--YNHLDFIWMADAPQEVYN 386

RESULT 11
Q9D760
ID Q9D760 PRELIMINARY; PRT; 395 AA.
AC Q9D760;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2310051B21Rik protein.
GN 2310051B21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weiss C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaiji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009560; BAB26359.1; -.
DR MGD; WGI:1914967; 2310051B21Rik.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44885 MW; FEF96B5EA670BEE CRC64;

Query Match 49.1%; Score 1049.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 2.1e-78;
Matches 195; Conservative 67; Mismatches 124; Indels 3; Gaps 3;

Qy 2 MWLLTTTCLICGTLNAGGFLDLENEVPVMTSEIIYNGYSEYEVTTEDGYILL 61
Db 1 MWLLLVTS-VLSAFGAGHGLFGKLPKPEANMNVSQMITYWGYPSEYEVTTEDGYILG 59
Qy 62 VNRIPIYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMWGNRSR 121
Db 60 VYRIPIYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMWGNRSR 119
Qy 122 NTSRRHKTLSDEKFWAFSDEMAYKDYLPVIDFIVNKTQGEKLYFIGHSLGTTIGFV 181
Db 120 NTSRRKNNVYSPDSVEFWAFSDEMAYKDYLPVIDFIVNKTQGEKLYFIGHSLGTTIGFV 179
Qy 182 AFSTMPALAKIKREYALAPVATVRYTESPFKKISLIPKFLKLVIFGNKMFPHNYLDQF 239
Db 180 AFSTMPALAKIKREYALAPVATVRYTESPFKKISLIPKFLKLVIFGNKMFPHNYLDQF 239
Qy 242 ASTKICNNKILWLICSEFMSLWAGSNKKNQSDVMYSHAPTSVSSVNIHLIKOLYHS 301
Db 240 LGTEVCSRELLDLCSNALIFCGFDKKNLNVRSRGVTLGHNPAGTSTQDLFHWLAQLAKS 299
Qy 302 DEFRAVDGNADNMKNHYNQSHPIYDLTAMKVPYTAIWAGGHDVLTGTPQDVARIILPOIKS 361
Db 300 GKLYANNNGSLQNLMLHYNQKTPPYDVSAMTVPYAVWNGGHDILADPDQVAMLLPKLPN 359
Qy 362 LSLVLSLPEWPTDFVWGLDAPORMFS 390
Db 360 LLYHKEILP--YNHLDFIWMADAPQEVYN 386

RESULT 12
Q9D766
ID Q9D766 PRELIMINARY; PRT; 395 AA.
AC Q9D766;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2310051B21Rik protein.
GN 2310051B21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaïdo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Offelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gysincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Ringwald M., Rodriguez I., Sakamoto N.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009544; BAB26350.1; -.
DR MGD: MGI:1914967; 2310051B21Rik.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00561; abhydrolase; 1.
DR PROSITE: PS00120; LIPASE_SER; 1.
DR SEQUENCE 395 AA; 44648 MW; CC69875653AA7A74 CRC64;

Query Match 49.1%; Score 1048.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 2.5e-78;
Matches 195; Conservative 65; Mismatches 126; Indels 3; Gaps 2;

Qy 2 MWLLTTTCCLICGTNAGFLDLENEVPVWMTSEIIYNGYPSEEVETEDGYILL 61
Db 1 MWLLLVTS-VLSAFGAHGLFGKLGPKNPANNNVSMQITYMGYPSEEVETEDGYILG 59

Qy 62 VNRIPTYGTHARSTGRPVVYMQHALFADNAYWLENYANGSLGFLIADAGYDVWNGNSRG 121
Db 60 VYRIPTYGKNSENICKRPVAYLQHGLIASATNWTNLPNNSLAFILADAGYDVWNGNSRG 119

Qy 122 NTWSRRHKTLSSTDCKFWAFSDEMAKYDLPGVDFIVNKTQOEKLYFTGHSLGTIGFV 181
Db 120 NTWSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVQKTQOEKIHYVGHSGQTIGFI 179

Qy 182 AFSTWPELAQRKMNPFALGPTISFYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFSTNPALAKKIKRYALAPVATVYTESPFKKISLIXFLKLVIFGNKMFMPYNVLDQF 239

Qy 242 ASTKICNNKILWLCSEFMSLWAGSNKKNMOSRMDVYMSHAPTSSVHNIIHKLQYHS 301
Db 240 LGTEVCSRELLDLCSNALFICFGDKKNLVSRFDVILGHNPAGTSTQDLPHWAQLAKS 299

Qy 302 DEFRAIDGNDADNKHYNQSHPIYDLTAMKVPTAIWAGGHVILGTPODVARIILPQIKS 361
Db 300 GKLIQAYNGWSPLQNNLHYNQKTPPYDVVSAMTVPIAVWNGGHDILADPDVAMLLPKLPN 359

Qy 362 LSLVLSLLPEWETDFVWGLDAPQMFS 390
Db 360 LLYHKELP--YNHLDIFWAMDAPQEVYN 386

RESULT 14
Q9D796 PRELIMINARY; PRT; 395 AA.
ID Q9D796
AC Q9D796;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:2310063K07, full insert sequence.
GN 2310051B21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN-C57BL/6J; TISSUE-TONGUE;
RX MEDLINE=35781; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavani H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gysincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK010026; BAB26651.1; -.
DR MGD: MGI:1914967; 2310051B21Rik.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00561; abhydrolase; 1.
DR PROSITE: PS00120; LIPASE_SER; 1.
DR SEQUENCE 395 AA; 44650 MW; 03F16D53373A4D57 CRC64;

Query Match 49.1%; Score 1048.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 2.5e-78;
Matches 195; Conservative 65; Mismatches 126; Indels 3; Gaps 2;

Qy 2 MWLLTTTCCLICGTNAGFLDLENEVPVWMTSEIIYNGYPSEEVETEDGYILL 61
Db 1 MWLLLVTS-VLSAFGAHGLFGKLGPKNPANNNVSMQITYMGYPSEEVETEDGYILG 59

Qy 62 VNRIPTYGTHARSTGRPVVYMQHALFADNAYWLENYANGSLGFLIADAGYDVWNGNSRG 121
Db 60 VYRIPTYGKNSENICKRPVAYLQHGLIASATNWTNLPNNSLAFILADAGYDVWNGNSRG 119

Qy 122 NTWSRRHKTLSSTDCKFWAFSDEMAKYDLPGVDFIVNKTQOEKLYFTGHSLGTIGFV 181
Db 120 NTWSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVQKTQOEKIHYVGHSGQTIGFI 179

Qy 182 AFSTWPELAQRKMNPFALGPTISFYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFSTNPALAKKIKRYALAPVATVYTESPFKKISLIXFLKLVIFGNKMFMPYNVLDQF 239

Qy 242 ASTKICNNKILWLCSEFMSLWAGSNKKNMOSRMDVYMSHAPTSSVHNIIHKLQYHS 301
Db 240 LGTEVCSRELLDLCSNALFICFGDKKNLVSRFDVILGHNPAGTSTQDLPHWAQLAKS 299

Qy 302 DEFRAIDGNDADNKHYNQSHPIYDLTAMKVPTAIWAGGHVILGTPODVARIILPQIKS 361
Db 300 GKLIQAYNGWSPLQNNLHYNQKTPPYDVVSAMTVPIAVWNGGHDILADPDVAMLLPKLPN 359

Qy 362 LSLVLSLLPEWETDFVWGLDAPQMFS 390
Db 360 LLYHKELP--YNHLDIFWAMDAPQEVYN 386

RESULT 14
Q9D796 PRELIMINARY; PRT; 395 AA.
ID Q9D796
AC Q9D796;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:2310063K07, full insert sequence.
GN 2310051B21Rik.
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009437; BAR26287.1; -
DR MGD: MGI:1914967; 2310051B21Rik.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00561; abhydrolase_1.
DR PROSITE: PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44684 MW; E9FB6AE85A81257F CRC64;

Query Match 49.0%; Score 1046.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 3.7e-78;
Matches 195; Conservative 64; Mismatches 127; Indels 3; Gaps 2;

QY 2 MWLLTTTCLICGTLNAGGFLDLENEVPEVMNTSEIIYNGYPSSEYEVTTEDGYILL 61
Db 1 MWLLLVTS-VLSAFGGAHGLFGKLGPKNPEANMNVSMQITYGYPSEYEVTTEDGYILG 59

QY 62 VNRIPTYGTHARSTGRPRVYVMQHALFADNAYWLENYANGSLGFLADAGYDVMGNRSRG 121
Db 60 VYRIPTYGKKNSENIGKRPVAYLQHLGLASATNWIINLPNNSLAFILADAGYDVMGNRSRG 119

QY 122 NTWSRRHKTSETDEKFWAFSFDMAKYDLPVDFIVNKTGQEKLYFIGHSLGTIGFV 181
Db 120 NTWSRKNVYSPDSVEFWAFSFDMAKYDLPATDFIVQKTGQEKIHYVGHSGQTIGFI 179

QY 182 AFSTWPELAQRKKNFALGPTISFYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFSTNPALAKKIKRFYALAPVATVKYTESPPKISLPKFLKVFIGNKMFPHNYLDQF 239

QY 242 ASTKICNKKILWLICSEFMSLWAGSNKKNMOSRMDVYMHAPTGSSVHNILHLKQLYHS 301
Db 240 LGTEVCSRELLDLCSNALFFCFGDFKKNLNVSRFDVYXGHNPGACTSTQDLFWHAQLAKS 299

QY 302 DEFAYDWGNDADNKKYNSHPPIYDLTAMKVPTAIWAGGHDVLTGPQDVARTILPOIKS 361
Db 300 GKLYQNWGSPQLNKLHYNQKTPPYDVSAMTVPVIAVWNGGHDILADPDQVAMLLPKLPN 359

QY 362 LSLVLSLLPEWPTDFVWGLDAPQRMFS 390
Db 360 LLXHKELP--YNHLDFIWMDAPQEVYN 386

RESULT 15
Q9D6Q3 PRELIMINARY; PRT; 395 AA.
ID Q9D6Q3

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AC Q9D6Q3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:2310068C02, full insert sequence.
GN 2310051B21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK010103; BAR26703.1; -
DR MGD: MGI:1914967; 2310051B21Rik.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00561; abhydrolase_1.
DR PROSITE: PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44638 MW; 4E52613BC98B3F CRC64;

Query Match 48.9%; Score 1045.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 4.4e-78;
Matches 195; Conservative 63; Mismatches 128; Indels 3; Gaps 2;

QY 2 MWLLTTTCLICGTLNAGGFLDLENEVPEVMNTSEIIYNGYPSSEYEVTTEDGYILL 61
Db 1 MWLLLVTS-VLSAFGGAHGLFGKLGPKNPEANMNVSMQITYGYPSEYEVTTEDGYILG 59

QY 62 VNRIPTYGTHARSTGRPRVYVMQHALFADNAYWLENYANGSLGFLADAGYDVMGNRSRG 121
Db 60 VYRIPTYGKKNSENIGKRPVAYLQHLGLASATNWIINLPNNSLAFILADAGYDVMGNRSRG 119

QY 122 NTWSRRHKTSETDEKFWAFSFDMAKYDLPVDFIVNKTGQEKLYFIGHSLGTIGFV 181
Db 120 NTWSRKNVYSPDSVEFWAFSFDMAKYDLPATDFIVQKTGQEKIHYVGHSGQTIGFI 179

QY 182 AFSTWPELAQRKKNFALGPTISFYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFSTNPALAKKIKRFYALAPVATVKYTESPPKISLPKFLKVFIGNKMFPHNYLDQF 239

QY 242 ASTKICNKKILWLICSEFMSLWAGSNKKNMOSRMDVYMHAPTGSSVHNILHLKQLYHS 301
Db 240 LGTEVCSRELLDLCSNALFFCFGDFKKNLNVSRFDVYXGHNPGACTSTQDLFWHAQLAKS 299

QY 302 DEFAYDWGNDADNKKYNSHPPIYDLTAMKVPTAIWAGGHDVLTGPQDVARTILPOIKS 361
Db 300 GKLYQNWGSPQLNKLHYNQKTPPYDVSAMTVPVIAVWNGGHDILADPDQVAMLLPKLPN 359

QY 362 LSLVLSLLPEWPTDFVWGLDAPQRMFS 390

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Db 360 LLYHKEILP--YNHLDFTWMDAPQEVYN 386

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Job time : 97 secs